



Db 193 PLYLGGVQLEKGRDLRLSAEINRPDYLDFAESGQVYFG 229

## RESULT 10

154490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C&gt;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C:Accession: 154490

R:Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus

A:Reference number: 154490; MUID:92218012

A:Accession: 154490

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 &lt;RES&gt;

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: PLTNF

A:Introns: 62/3; 81/1; 97/1

Superfamily: tumor necrosis factor

Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 7.9%; Score 132.5; DB 2; Length 235;

Best Local Similarity 25.3%; Pred. No. 0.0011; Indels 43; Gaps 7;

Matches 42; Conservative 27; Mismatches 54; Indels 43; Gaps 7;

Qy 163 OPFAHLTINATDIPSGSHKVSLSWYHGRGAKISNMTFSNG-----KLIYNODGFYVL 216

Db 90 KPAHVAN-----HQVDQLEWLSRG-----ANALLANGMOLKDNQVLPADGLYLIV 137

Qy 217 YANICFRHETSGDLATEYLQLMVYTK-----TSIKIPSSHTLMKGGSTYK 264

Db 138 YSOVLK-----GQCSSYVLLTHVSPAVSYEDKVNLSAISKPCPKETPEGSSELKPW 192

Qy 265 SCNSEFHYISINVGGFKLRSEIEISVNSPLLD-PPDQATYFG 309

Db 193 -----YEPYILGGVQLEKGRDLRLSAEINRPDYLDFAESGQVYFG 231

## RESULT 11

JU0029

tumor necrosis factor alpha precursor - rat

N:Alternate names: cachectin; TNF alpha

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Feb-2000

C:Accession: JU0029; JN0868; S21674

Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.

Viric. Biol. Chem. 53, 1733-1736, 1989

A:Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor

A:Reference number: JU0029.

A:Accession: JU0029

A:Molecule type: DNA

A:Residues: 1-235 &lt;SHI&gt;

R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.

Gene 132, 227-236, 1993

A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.

A:Reference number: JN0868; MUID:94040766

A:Accession: JN0868

A:Molecule type: DNA

A:Residues: 1-235 &lt;KWO&gt;

A:Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254

R:Exler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.

Biol. Chem. Hoppe-Seyler 373, 271-281, 1992

A:Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro

A:Reference number: S21674; MUID:92329007

A:Accession: S21674

A:Molecule type: mRNA

A:Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 &lt;EST&gt;

A:Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370

C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

F:80-235/Product: tumor necrosis factor #status predicted &lt;MAT&gt;

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:148-179/Disulfide bonds: #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 235;

Best Local Similarity 25.3%; Pred. No. 0.0013;

Matches 41; Conservative 27; Mismatches 59; Indels 35; Gaps 7;

Qy 163 OPFAHLTINATDIPSGSHKVSLSWYHGRGAKISNMTFSNGKLIYNODGFYVLXANI 220

Db 90 KPAHVAN-----HQVDQLEWLSRG-----ANALLANGMOLKDNQVLPADGLYLIVSQV 141

Qy 221 CFRHETSGDLATEYLQLMVYTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268

Db 142 LFK-----GQCDDVLLTHVSPAVSYEDKVNLSAISKPCPKDTEGALKPW----- 192

Qy 269 EFHYISINVGGFKLRSEIEISVNSPLLD-PPDQATYFG 309

Db 193 ---YEPYILGGVQLEKGRDLRLSAEINRPDYLDITSGQVYFG 231

## RESULT 12

I49139

lymphotoxin-beta - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I49139; I49138; I49076

R:Lawton, P.; Nelson, J.; Tizard, R.; Browning, J.L.

J. Immunol. 154, 239-246, 1995

A:Title: Characterization of the mouse lymphotoxin-beta gene.

A:Reference number: I49138; MUID:95088371

A:Accession: I49139

A&gt;Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-306 &lt;RES&gt;

A:Cross-references: EMBL:U16985; NID:g577830; PIDN:AAA70089.1; PID:g577831

A:Accession: I49138

A&gt;Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-306 &lt;RES&gt;

A:Cross-references: EMBL:U16984; NID:g577431; PIDN:AB60493.1; PID:g577432

R:Polholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov, S.V.; N.

Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995

A:Title: Cloning and expression analysis of the murine lymphotoxin beta gene.

A:Reference number: A55602; MUID:95148600

A:Accession: I49076

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-306 &lt;RE2&gt;

A:Cross-references: EMBL:U12029; NID:g515508; PIDN:AAA67716.1; PID:g515509

C:Genetics:

A:Gene: LT-beta

A:Introns: 54/3; 160/1

Query Match

Best Local Similarity 22.1%; Pred. No. 0.0023;

Matches 55; Conservative 38; Mismatches 87; Indels 69; Gaps 12;

Qy 105 ESQDTKLIP---DSCRRKQAFQAGVQKELQHVQSHIRAEKAMVDGSGWLDLAKRSKLE 161

Db 86 ETPDPRLHPQRSNAGRNLAISTSQGPV-----AQSREASAMMTI----- 124

Qy 162 AOPFAHLTIN--ATDIPSGSHKVSLS-----SWYHGRG--WAKISNTTF----- 201

Db 125 LSPAADSTPDGVOQLPKGEPTDLNPELPAHLIGAMNSGGGLSWEASQEAFLRSQAQ 184

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho  
F:1-77/Domain: propeptide #status predicted <PRO>  
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
F:80/Binding site: myristate (Lys) (covalent) #status predicted  
F:82/Binding site: myristate (Ser) (covalent) #status predicted  
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:146-178/Disulfide bonds: #status predicted

Query Match 8.1%; Score 137; DB 1; Length 234;  
Best Local Similarity 26.1%; Pred. No. 0.00046;  
Matches 52; Conservative 30; Mismatches 71; Indels 46; Gaps 10;

QY 134 IVGSHIRAEKAMVDSW---LDLAKRSKLEA---OPFAHLTINATIPSGSHKVSLSGSW 187  
DB 55 VIGPQ--REQSPAGSFNPLVQVTLRSSQASNNKPVHVVAN-----ISAP 100  
QY 188 YHNRGWAKISNTFNG-----KLIVNODGYIYLYANTCFRHH-----TSGDL 231  
101 GOLRWGDSYANALMANGVELKDNQLVVPTDGLYISQVLFGRHGPCSTPLFTHTISRI 160  
QY 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYVSGNSEHFYSINVGFFKLSRSEESI 291  
DB 161 AVSY-OTKVNIL-SAIKSPCHRETLEGARKPW-----YEPYOGGVFOLEKGRLSA 211  
QY 292 EVSNPSLLD-PQDATYFG 309  
DB 212 EINLPELYAESGQVYFG 230

RESULT 9  
QWUHN  
tumor necrosis factor alpha precursor [validated] - human  
N:Alternate names: cachectin; TNFA  
C:Species: Homo sapiens (man)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Dec-2000  
C:Accession: A93585; S36153; A44189; B61478; I53311; S62610; I54522; A01646; B23  
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D  
Nucleic Acids Res. 13, 6361-6373, 1985  
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr  
A:Reference number: A93585; MUID:86016093  
A:Accession: A93585  
A:Molecule type: DNA  
A:Residues: 1-233 <NED>  
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
R:Iriss, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka  
Nature Genet. 3, 137-145, 1993  
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a  
Reference number: S36152; MUID:93272029  
A:Accession: S36153  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-233 <IRI>  
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992  
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.  
Nature 312, 724-729, 1984  
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to I  
A:Reference number: A93351; MUID:85086244  
A:Accession: A93351  
A:Molecule type: mRNA  
A:Residues: 1-233 <PEN>  
A:Cross-references: GB:X02910; NID:g37209; PIDN:CAA26669.1; PID:g37210  
A:Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloc  
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;  
Science 228, 149-154, 1985  
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A:Reference number: A44189; MUID:85142190  
A:Accession: A44189  
A:Molecule type: mRNA  
A:Residues: 1-62, 'S', 64-233 <WAN>  
A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738  
R:Fukuda, S.; Ando, O.; Tanai, M.; Masaki, N.; Nakamura, K.I.; An  
Lymphokine Res. 7, 175-185, 1988

A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta  
A:Reference number: A61478; MUID:88301617  
A:Accession: B61478  
A:Molecule type: protein  
A:Residues: 83-102;109-119;121-128, 'X',130-131;142-144, 'X',146, 'XXX',150-152;159-174  
R:Mamenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawasaki  
Eur. J. Biochem. 152, 515-522, 1985  
A:Title: Molecular cloning and expression of human tumor necrosis factor and compari  
A:Reference number: I53311; MUID:86030296  
A:Accession: I53311  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-233 <MAR>  
A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
A:Experimental source: U-937 cells S.; Fukuda, S.; Kurimoto, M.  
R:Takura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
Eur. J. Biochem. 235, 431-437, 1996  
A:Title: O-Glycosylated species of natural human (tumor-necrosis factor-alpha.  
A:Reference number: S62610; MUID:96202967  
A:Accession: S62610  
A:Molecule type: protein  
A:Residues: 77-99 <AK>  
R:D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter  
A:Reference number: I54522; MUID:94102809  
A:Accession: I54522  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8 <DAL>  
A:Cross-references: GB:S68530; NID:G544751  
R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992  
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific  
A:Reference number: A59163; MUID:93018920  
A:Contents: annotation; identification of myristylated lysines  
R:Agarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Hensel, W.J.; B  
J. Biol. Chem. 260, 2345-2354, 1985  
A:Title: Human tumor necrosis factor. Production, purification, and characterization  
A:Reference number: A92511; MUID:85130974  
A:Contents: annotation; disulfide bond  
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc  
out detriment to normal cells. It can also act synergistically with interferon gamma  
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clic  
ut are produced by different cell types and have different induction kinetics.  
C:Genetics:  
A:Gene: GDB:TNF; TNFA  
A:Cross-references: GDB:120441; OMIM:191160  
A:Map position: 6p21.3-6p21.3  
A:Introns: 62/3; 78/1; 94/1  
C:Complex: homotrimer  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine;  
F:1-76/Domain: propeptide #status predicted <PRO>  
F:77-233/Product: tumor necrosis factor #status experimental <MAT>  
F:19-20/Binding site: myristate (Lys) (covalent) #status experimental  
F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental  
F:145-177/Disulfide bonds: #status experimental

Query Match 7.9%; Score 133; DB 1; Length 233;  
Best Local Similarity 25.5%; Pred. No. 0.00099;  
Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

QY 163 QPFAHLTINATIPSGSHKVSLSWYHGRWAKISN-MTFSNGLKLVNODGYLYANIC 221  
DB 87 KPVHVVAN---PQAEGL---QWLNRRNALLANGVELRDLQVVPSEGLYISQVL 139  
QY 222 FRHH--ETSGDLATEYLQLMV--YVTK-----TSIKIPSSHTLMKGGSTKYVSGNSEHFY 273  
DB 140 FRGQCPSTHLLTHTTISRIVSYOTKVLLSAIKSPQRETPEGAAPW-----YE 192  
QY 274 SINVGFFKLSRSEESIYSVNPSSLLD-PQDATYFG 309

A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-230, 'R', 232-235 <RES>  
A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA0457.1; PID:g202083  
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A:Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor  
A:Reference number: A36696; MUID:91097531  
A:Accession: A36696  
A:Molecule type: protein  
A:Residues: 80-85, 'X', 87-99 <SHE>  
C:Genetics:  
A:Introns: 62/3; 81/1; 97/1  
A:Note: the first intron occurs in the 5'-untranslated region  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane  
F:80-235/Product: tumor necrosis factor status experimental <MAT>  
F:80/Binding site: myristate (Lys) (covalent) #status predicted  
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:148-179/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141.5; DB 1; Length 235;  
Best Local Similarity 25.9%; Pred. No. 0.00019;  
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

QY 163 QPFAHITINATDIPSGSHKVSLS-SWYHGRGAKISN-WTFNSGKLIVNODGFYLYYANI 220  
Db 90 KPAHVAVN-----HQVEQLEWLSQRANALLANGMDLNQNVADGILYISQV 141  
QY 221 CFRHHETSGDLATEYLQLMVYTK-----TSIKIPSSHTLMRGSGTKYWSGNS 268  
Db 142 LFK-----CGCPDYVLLHTVSRFAISYQKVNLSAVKSPCKDTPGEALKPW---- 192  
QY 269 EFHFTSINVGPFKLRSGEISIEVSNPSLLD-PDQATYFG 309  
Db 193 ---YEPIYLGGVFQLEKQDLSAEVNLPKYLDPAESGQVYFG 231

RESULT 7  
A25451  
tumor necrosis factor alpha precursor - rabbit  
N:Alternate names: cachectin; TNF alpha  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
C:Accession: A25454; A25451; JS0727  
R:Itto, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.  
DNA 5, 149-156, 1986  
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor alpha  
A:Reference number: A25454; MUID:86219711  
A:Accession: A25454  
A:Molecule type: mRNA  
A:Residues: 1-234 <ITO>  
A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760  
R:Itto, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
DNA 5, 157-165, 1986  
A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
A:Reference number: A25451; MUID:86219712  
A:Accession: A25451  
A:Molecule type: DNA  
A:Residues: 1-234 <ITO>  
A:Note: this sequence differs from that shown in having a Gln inserted between residues R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
Gene 95, 215-221, 1990  
A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- $\alpha$  and TNF- $\beta$   
A:Reference number: JH0309; MUID:91065534  
A:Accession: JS0727  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-62, 'Q', 63-234 <SHA>  
A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756  
C:Genetics:  
A:Introns: 62/3; 80/1; 96/1

C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane  
F:1-81/Domain: propeptide #status predicted <PRO>  
F:82-234/Product: tumor necrosis factor status predicted <MAT>  
F:82/Binding site: myristate (Lys) (covalent) #status predicted  
F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:147-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;  
Best Local Similarity 21.6%; Pred. No. 0.00021;  
Matches 65; Conservative 35; Mismatches 99; Indels 102; Gaps 13;

QY 27 EGPLHAPPPAPHPAPASR-----SMFVALIGLIGGVVCSVALFFYFRAQMDPNRISD 82  
Db 14 EGPL-----PKAGGPGSKRCCLSLFSLVAGATLFC-----LLHFRVIGQEEESP 65  
QY 83 GTHCYIRILRLHENADFOTTLTESQDTKLIPDSRCRIKQAFQAGVOKELQHVGSQHIRA 142  
Db 66 NUHLV-----NPVQAWTLRS-----A 82  
QY 143 EKAVDGSWLDLAKRSKLEAQPFAHITINATDIPSGSHKVSLSWYHGRGAKISN-WTF 201  
Db 83 SRALSD-----KPLAHVVAN-----PQVEGQL-----OWLSORANALLANGMKL 121  
QY 202 SNKKLVNODGFYLYYANICFRHHETSGDLATEYLQLMVYTKTSIKIPSSHTLMKG--- 258  
Db 122 TDNLQVVPADGLYLYISQVLF-----SGGCRSYVLLTHTVSRFAVSPYKVNLLSAIKS 176  
QY 259 -----GSTKYWSGNESEFHYISNVGGFKLRSGEISIEVSNPSLLD-PDQATYF 308  
Db 177 PCURETPEEAEPMAW-----YEPIYLGGVFQLEKGRDLSTEVNQPYLEDLAESGQVYF 229  
QY 309 G 309  
Db 230 G 230

RESULT 8  
JH0529  
tumor necrosis factor alpha precursor - sheep  
N:Alternate names: cachectin; TNF alpha  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
C:Accession: JH0529; S48118; S13114; S20661  
R:Green, I.R.; Sargan, D.R.  
Gene 109, 203-210, 1991  
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with the reference sequence  
A:Reference number: JH0529; MUID:92112044  
A:Accession: JH0529  
A:Molecule type: mRNA  
A:Residues: 1-234 <GRE>  
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406  
R:Nash, A.D.; Baruch, G.J.; Brandon, M.R.; Andrews, A.E.  
Immunol. Cell Biol. 69, 273-283, 1991  
A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.  
A:Reference number: S48118; MUID:92155784  
A:Accession: S48118  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-234 <NAS>  
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807  
R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.  
Nucleic Acids Res. 18, 6723, 1990  
A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.  
A:Reference number: S13114; MUID:91067496  
A:Accession: S13114  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-62, 64-234 <YOD>  
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404  
A:Note: comparison with the introns of homologous sequences suggest that this is prot  
C:Superfamily: tumor necrosis factor



[illegible]

## RESULT 6

C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Apr-2001  
C:Accession: S28017; JH0793; S26694; S28852; 153476; S25684; S30593  
R:Holtenbaug, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; BO J. 11, 4313-4321, 1992  
A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for BO J. 11, 4313-4321, 1992  
A:Reference number: S28017; MUID:93049181  
A:Accession: S28017  
A:Molecule type: mRNA  
A:Residues: 1-261 <HOL>  
A:Cross-references: EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484  
R:Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T. J. Exp. Med. 176, 1543-1550, 1992  
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin secretion  
A:Reference number: JH0793; MUID:93094757  
A:Accession: JH0793  
A:Molecule type: mRNA  
A:Residues: 1-261 <SPR>  
A:Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412  
R:Experimental source: peripheral blood T-cell  
R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A. Eur. J. Immunol. 22, 3191-3194, 1992  
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
A:Reference number: S26694; MUID:93076854  
A:Accession: S26694  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-261 <GRA>  
A:Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270  
R:Gauchat, J.P.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J. FEBS Lett. 315, 259-266, 1993  
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of expression  
Reference number: S28852; MUID:93138085  
Accession: S28852  
A:Molecule type: mRNA  
A:Residues: 1-261 <GAU>  
A:Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124  
A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln  
C:Genetics:  
A:Gene: GDB:CD40LG; HIGM1; IMD3  
A:Cross-references: GDB:120632; OMIM:308230  
A:Map position: Xq26-Xq26  
C:Keywords: glycoprotein; transmembrane protein  
F:13-44/Domain: transmembrane #status predicted <TMM>  
F:45-261/domain: extracellular #status predicted <EXT>  
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;  
Best Local Similarity 24.5%; Pred. No. 8.1e-06;  
Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

Qy	45	SRSMFVALLGLL-QQWCVSVALFFPRAQMDPNRISDGTGTHCIYRILRLHENAQDPDR-	102
Db	20	SMKIFMYLLAVELITOMIGSALFAYVLRRLD-KIEDE-----RNHDEVFPMKTI	69
Qy	103	-TLESQDTKLIPDSRRIKQAQFQAVOKELQHVGSQHRAERAMVDGSLDLAKRSKLE	161
Db	70	QRCTGSRSLNLCERIKSQFQGFV-KDYM-----LNKEETKENSFEMOKGDO-N	119

## RESULT 6

C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Apr-2001  
C:Accession: S28017; JH0793; S26694; S28852; 153476; S25684; S30593  
R:Holtenbaug, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; BO J. 11, 4313-4321, 1992  
A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for BO J. 11, 4313-4321, 1992  
A:Reference number: S28017; MUID:93049181  
A:Accession: S28017  
A:Molecule type: mRNA  
A:Residues: 1-261 <HOL>  
A:Cross-references: EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484  
R:Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T. J. Exp. Med. 176, 1543-1550, 1992  
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin secretion  
A:Reference number: JH0793; MUID:93094757  
A:Accession: JH0793  
A:Molecule type: mRNA  
A:Residues: 1-261 <SPR>  
A:Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412  
R:Experimental source: peripheral blood T-cell  
R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A. Eur. J. Immunol. 22, 3191-3194, 1992  
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
A:Reference number: S26694; MUID:93076854  
A:Accession: S26694  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-261 <GRA>  
A:Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270  
R:Gauchat, J.P.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J. FEBS Lett. 315, 259-266, 1993  
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of expression  
Reference number: S28852; MUID:93138085  
Accession: S28852  
A:Molecule type: mRNA  
A:Residues: 1-261 <GAU>  
A:Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124  
A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln  
C:Genetics:  
A:Gene: GDB:CD40LG; HIGM1; IMD3  
A:Cross-references: GDB:120632; OMIM:308230  
A:Map position: Xq26-Xq26  
C:Keywords: glycoprotein; transmembrane protein  
F:13-44/Domain: transmembrane #status predicted <TMM>  
F:45-261/domain: extracellular #status predicted <EXT>  
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;  
Best Local Similarity 24.5%; Pred. No. 8.1e-06;  
Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

Qy	45	SRSMFVALLGLL-QQWCVSVALFFPRAQMDPNRISDGTGTHCIYRILRLHENAQDPDR-	102
Db	20	SMKIFMYLLAVELITOMIGSALFAYVLRRLD-KIEDE-----RNHDEVFPMKTI	69
Qy	103	-TLESQDTKLIPDSRRIKQAQFQAVOKELQHVGSQHRAERAMVDGSLDLAKRSKLE	161
Db	70	QRCTGSRSLNLCERIKSQFQGFV-KDYM-----LNKEETKENSFEMOKGDO-N	119

Query Match	10.5%	Score 176.5;	DB 2;	Length 261;
Best-Local Similarity	24.2%	Pred. No. 2.5e-07;		
Matches	70;	Conservative 54;	Mismatches 122;	
			Indels 43;	Gaps 13;

Qy	150	SWLDLAKRSKLEAOPNAHLTINATDIPSCGSHKVSLSNWDHGWAKISN--MTFSNCK-L 200
Db	113	-----MHKGQEPQIAARVISENS-----SKTTSVLQW-APKYYITLSNNLYTLENGKQL 161
Qy	207	IVNODGYFYIYANICFRHHFTSGDLATEYLQLMVYVYTTTSIKIP--SSHTLMKGGSFYKW 264
Db	162	AVKRGQGYIYITQVTCNSR-----EYLSQAPFIASLCKLSPSGSERILLRAANTH-- 212
Qy	265	SGNSERHFYINVGGFYKFLRSGEISIEVSNPSNLDLPQODATYFGAFV 313
Db	213	SSSRPCGQOQTHLGGVFELQSGASVFVNVTDPSQVSHGTFGTFSGLLAKL 261

Query Match	10.4%	Score 175.5;	DB 2;	Length 278;
Best Local Similarity	20.3%	Pred. No. 3.3e-07;		
Matches	64:	Conservative	47:	Mismatches 106:
				Indels 99:
				Gaps 10:

[illegible]

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 56.3343 Seconds  
(without alignments)  
540.706 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1695  
Sequence: 1 MRRASRDYTKYLGSEMGG.....LLDPDQATYFGAFKVRDID 317

Scoring table: BLASUM62  
Gapop 10.0 , Gapext 0.5

Archived: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	11.2	281	2	Fas ligand - human
2	184.5	10.9	279	2	Fas ligand - mouse
3	176.5	10.5	261	2	CD40 ligand - bovi
4	175.5	10.4	278	2	fas ligand - rat
5	158.5	9.4	261	2	CD40 ligand - huma
6	141.5	8.4	235	1	tumor necrosis fac
7	141	8.4	234	1	tumor necrosis fac
8	137	8.1	234	1	tumor necrosis fac
9	133	7.9	233	1	tumor necrosis fac
10	132.5	7.9	233	1	tumor necrosis fac
11	131.5	7.8	235	2	tumor necrosis fac
12	130.5	7.7	306	2	lymphotoxin-beta -
13	130	7.7	233	1	tumor necrosis fac
14	128	7.6	234	1	tumor necrosis fac
15	126.5	7.5	233	1	tumor necrosis fac
16	126	7.5	232	1	tumor necrosis fac
17	125.5	7.4	185	2	tumor necrosis fac
18	122	7.2	193	2	tumor necrosis fac
19	120	7.1	260	2	CD40 ligand - mous
20	117	6.9	233	2	tumor necrosis fac
21	117	6.9	244	2	lymphotoxin beta -
22	97.5	5.8	1464	1	collagen alpha 1(I
23	94.5	5.6	664	2	probable protein k
24	92.5	5.5	205	1	lymphotoxin alpha
25	92.5	5.5	450	2	hypothetical prote
26	91.5	5.4	3848	2	TiPC protein - sli
27	91	5.4	493	2	probable GntR-fam
28	90.5	5.4	1694	2	sialoadhesin - mou
29	90	5.3	730	2	gelatinase B (EC 3

homoprotocatechuat  
farnesyl-protein t  
tumor necrosis fac  
glyceraldehyde-3-p  
fibrinogen beta ch  
probable two-compo  
hypothetical prote  
probable phosphoe  
leucine-rich repea  
heparan sulfate-N-  
galactinolactone d  
collagen alpha 1(I  
protein p1 - Entam  
125K surface anti  
hypothetical prote  
hypothetical prote

## ALIGNMENTS

### RESULT 1

I38707

Fas ligand - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C:Accession: I38707; JC2340; S57565; I38554

R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A:Title: Human Fas ligand; gene structure, chromosomal location and species specific

A:Reference number: I38707; MUID:95127560

A:Accession: I38707

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-281 <RES>

A:Cross-references: EMBL:U11821; NID:G595430; PIDN:AAC50124.1; PID:G595431

R:Mita, E.; Hayashi, N.; Ito, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto,

Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.

A:Reference number: JC2340; MUID:95071350

A:Accession: JC2340

A:Molecule type: DNA

A:Residues: 1-281 <MIT>

A:Cross-references: GB:D38122; DBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:G13699

R:Schatzlein, C.B.

submitted to the EMBL Data Library, June 1995

A:Reference number: S57565

A:Accession: S57565

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-281 <SCH>

A:Cross-references: EMBL:X89102; NID:G887455; PID:G887456

R:Allderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.

J. Exp. Med. 181, 71-77, 1995

A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.

A:Reference number: I38554; MUID:95105731

A:Accession: I38554

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-281 <RE2>

A:Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628

C:Genetics:

A:Gene: FasL

A:Introns: 151/1; 116/3

C:Keywords: glycoprotein; transmembrane protein

F:80-102/Domain: transmembrane #status predicted <TMM>

F:76,184,250,260/Binding site: carbohydrate (Asn) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;

Best Local Similarity 21.7%; Pred. No. 2.4e-08;

Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

QY 22 PGAPHEGFLHAPPAP-----HQPAAASRS-----MFVALLGLIGLGVQVCS 63

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (sf  
 N:Alternate names: 190K protein; polymorphic schizont antigen  
 C:Species: Plasmodium falciparum  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jun-2000  
 C:Accession: S06286  
 R:Certá, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.  
 EMBO J. 6, 4137-4142, 1987  
 A:Title: A naturally occurring gene encoding the major surface antigen precursor p190 of  
 A:Reference number: S06286; MUID:88166657  
 A:Accession: S06286  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-1060 <CER>  
 C:Superfamily: major merozoite surface antigen  
 C:Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1060;  
 Best Local Similarity 60.0%; Pred. No. 19;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 983 QFVKSNSKVITGLTE 997

#### RESULT 7

S16752  
 major merozoite surface antigen MSA-1 - malaria parasite (Plasmodium falciparum) (fragme  
 N:Alternate names: polymorphic schizont antigen p190  
 C:Species: Plasmodium falciparum  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jun-2000  
 C:Accession: A44865; S16752  
 R:Olafsson, P.; Matile, H.; Certá, U.  
 Exp. Parasitol. 74, 381-389, 1992  
 A:Title: Plasmodium falciparum: the repetitive MSA-1 surface protein of the RO-71 isolat  
 A:Reference number: A44865; MUID:92275047  
 A:Accession: A44865  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1086 <OLA>  
 A:Cross-references: EMBL:X61930  
 A:Experimental source: isolate RO-71  
 C:Genetics:

A:Gene: MSA1

C:Superfamily: major merozoite surface antigen

C:Keywords: glycoprotein; merozoite; surface antigen; tandem repeat

Query Match 57.4%; Score 42.5; DB 2; Length 1086;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 1009-QFVKSNSKVITGLTE 1023

DB 1009-QFVKSNSKVITGLTE 1023

DB 1009-QFVKSNSKVITGLTE 1023

DB 1009-QFVKSNSKVITGLTE 1023

DB 1009-QFVKSNSKVITGLTE 1023

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DB 1009-QFVKSNSKVITGLTE 1023

DB 1009-QFVKSNSKVITGLTE 1023

DB 1009-QFVKSNSKVITGLTE 1023

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (sf  
 N:Alternate names: 190K protein; polymorphic schizont antigen  
 C:Species: Plasmodium falciparum  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jun-2000  
 C:Accession: S06286  
 R:Certá, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.  
 EMBO J. 6, 4137-4142, 1987  
 A:Title: A naturally occurring gene encoding the major surface antigen precursor p190 of  
 A:Reference number: S06286; MUID:88166657  
 A:Accession: S06286  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-1060 <CER>  
 C:Superfamily: major merozoite surface antigen  
 C:Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1060;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

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DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (sf  
 N:Alternate names: 190K protein; polymorphic schizont antigen  
 C:Species: Plasmodium falciparum  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jun-2000  
 C:Accession: S06286  
 R:Certá, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.  
 EMBO J. 6, 4137-4142, 1987  
 A:Title: A naturally occurring gene encoding the major surface antigen precursor p190 of  
 A:Reference number: S06286; MUID:88166657  
 A:Accession: S06286  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-1060 <CER>  
 C:Superfamily: major merozoite surface antigen  
 C:Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1060;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

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DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (sf  
 N:Alternate names: 190K protein; polymorphic schizont antigen  
 C:Species: Plasmodium falciparum  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jun-2000  
 C:Accession: S06286  
 R:Certá, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.  
 EMBO J. 6, 4137-4142, 1987  
 A:Title: A naturally occurring gene encoding the major surface antigen precursor p190 of  
 A:Reference number: S06286; MUID:88166657  
 A:Accession: S06286  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-1060 <CER>  
 C:Superfamily: major merozoite surface antigen  
 C:Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1060;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

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DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKVITGLTE 997

DB 983 QFVKSNSKV

Thu Oct 10 16:31:18 2002

us-09-787-126-34.rpr

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA  
A;Residues: 1-123 <TAS>  
C;Superfamily: Immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.4%; Score 41; DB 2; Length 123;  
Best Local Similarity 64.3%; Pred. No. 3.9;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 YIKANSKFIGITEL 15  
DB 57 YIKYNERFKGTTTL 70

RESULT 14

H97146  
siderophore/surfactin synthetase related protein [imported] - Clostridium acetobutyli  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C;Accession: H97146  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: H97146  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-447 <KUR>  
A;Cross-references: GB:AE001437; PIDN:AAK79963.1; PID:915024986; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum AFCC824  
C;Genetics:  
A;Gene: CAC2004

Query Match 55.4%; Score 41; DB 2; Length 447;  
Best Local Similarity 63.6%; Pred. No. 15;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QYIKANSKFIG 11  
DB 291 KIIRNKRFIG 301

RESULT 15

G36812  
hypothetical protein ORF63 - saimiriine herpesvirus 1 (strain 11)  
C;Species: saimiriine herpesvirus 1  
A;Note: host Saimiri sciureus (common squirrel monkey)  
C;Date: 16-Oct-1992 #sequence\_revision 16-Oct-1992 #text\_change 08-Oct-1999  
C;Accession: G36812  
R;Albrecht, J.  
submitted to the EMBL Data Library, January 1992  
A;Description: Primary structure of the herpesvirus saimiri genome.  
A;Reference number: A36806  
A;Accession: G36812  
A;Molecule type: DNA  
A;Residues: 1-899 <ALB>  
A;Cross-references: GB:X64346; NID:960320; PIDN:CAA45686.1; PID:960384  
R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;  
J. Virol. 66, 5047-5058, 1992  
A;Title: Primary structure of the herpesvirus saimiri genome.  
A;Reference number: A37309; MUID:92333688  
A;Contents: annotation; protein-coding frames  
A;Note: neither protein nor nucleotide sequence is given  
C;Genetics:  
A;Gene: 63

Query Match 55.4%; Score 41; DB 2; Length 899;  
Best Local Similarity 50.0%; Pred. No. 30;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 127 KYQVARSKMIGSAEL 141

RESULT 13

G48677  
Ig heavy chain V-D-J region (419.1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C;Accession: G48677  
R;Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.  
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993  
A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibody  
A;Reference number: A48677; MUID:94022404  
A;Accession: G48677

Query Match 56.8%; Score 42; DB 2; Length 1333;  
Best Local Similarity 53.3%; Pred. No. 29;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 127 KYQVARSKMIGSAEL 141

RESULT 12

S38635  
blastopoda polyprotein - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 17-Nov-2000  
C;Accession: S38635  
R;Frommer, G.; Schuh, R.; Jdckle, H.  
submitted to the EMBL Data Library, November 1993  
A;Description: Localized expression of a novel microplasia-like element in the blastoderm  
A;Reference number: S38635  
A;Accession: S38635  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1333 <FRO>  
A;Cross-references: EMBL:227119; NID:g415797; PID:g415798  
C;Genetics:  
A;Gene: FlyBase:microplasia  
A;Cross-references: FlyBase:FBgn0014947  
C;Keywords: polyprotein

Query Match 57.4%; Score 42.5; DB 2; Length 1726;  
Best Local Similarity 60.0%; Pred. No. 31;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFIGITEL 14  
DB 1026 QPVKNSKVITGLTE 1040

A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-1726 <CHA>  
C;Cross-references: GB:M37213  
C;Superfamily: major merozoite surface antigen  
C;Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1726;  
Best Local Similarity 60.0%; Pred. No. 31;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFIGITEL 14  
DB 1026 QPVKNSKVITGLTE 1040

RESULT 12

S38635  
blastopoda polyprotein - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 17-Nov-2000  
C;Accession: S38635  
R;Frommer, G.; Schuh, R.; Jdckle, H.  
submitted to the EMBL Data Library, November 1993  
A;Description: Localized expression of a novel microplasia-like element in the blastoderm  
A;Reference number: S38635  
A;Accession: S38635  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1333 <FRO>  
A;Cross-references: EMBL:227119; NID:g415797; PID:g415798  
C;Genetics:  
A;Gene: FlyBase:microplasia  
A;Cross-references: FlyBase:FBgn0014947  
C;Keywords: polyprotein

Query Match 56.8%; Score 42; DB 2; Length 1333;  
Best Local Similarity 53.3%; Pred. No. 29;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 127 KYQVARSKMIGSAEL 141

RESULT 13

G48677  
Ig heavy chain V-D-J region (419.1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C;Accession: G48677  
R;Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.  
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993  
A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibody  
A;Reference number: A48677; MUID:94022404  
A;Accession: G48677

Query Match 56.8%; Score 42; DB 2; Length 1333;  
Best Local Similarity 53.3%; Pred. No. 29;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 127 KYQVARSKMIGSAEL 141

RESULT 12

S38635  
blastopoda polyprotein - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 17-Nov-2000  
C;Accession: S38635  
R;Frommer, G.; Schuh, R.; Jdckle, H.  
submitted to the EMBL Data Library, November 1993  
A;Description: Localized expression of a novel microplasia-like element in the blastoderm  
A;Reference number: S38635  
A;Accession: S38635  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1333 <FRO>  
A;Cross-references: EMBL:227119; NID:g415797; PID:g415798  
C;Genetics:  
A;Gene: FlyBase:microplasia  
A;Cross-references: FlyBase:FBgn0014947  
C;Keywords: polyprotein

Query Match 57.4%; Score 42.5; DB 2; Length 1726;  
Best Local Similarity 60.0%; Pred. No. 31;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFIGITEL 14  
DB 1026 QPVKNSKVITGLTE 1040

RESULT 12

S38635  
blastopoda polyprotein - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 17-Nov-2000  
C;Accession: S38635  
R;Frommer, G.; Schuh, R.; Jdckle, H.  
submitted to the EMBL Data Library, November 1993  
A;Description: Localized expression of a novel microplasia-like element in the blastoderm  
A;Reference number: S38635  
A;Accession: S38635  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1333 <FRO>  
A;Cross-references: EMBL:227119; NID:g415797; PID:g415798  
C;Genetics:  
A;Gene: FlyBase:microplasia  
A;Cross-references: FlyBase:FBgn0014947  
C;Keywords: polyprotein

OY 1 QYIKANSKFIGITE 14  
Db 124 QYITSNATFTGISE 137

Search completed: October 10, 2002, 15:59:14  
Job time : 5.66566 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 2.66566 Seconds  
(without alignments)  
540.706 Million cell updates/sec

Title: US-09-787-126-34

Perfect score: 74

Sequence: 1 QVIKANSFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	1315	1 BTCLTN	tentoxylisin (EC 3
2	44.5	60.1	244	2 S29982	class II histocomp
3	44	59.5	66	2 S31029	gene 84 protein -
4	43	58.1	180	2 G86826	diamine N-acetyltr
5	43	58.1	899	2 T42976	hypothetical prote
6	42.5	57.4	1060	2 S06286	major merozoite su
7	42.5	57.4	1086	2 S16752	major merozoite su
8	42.5	57.4	1701	2 A54498	major merozoite su
9	42.5	57.4	1701	2 A26868	major merozoite su
10	42.5	57.4	1726	1 SAZOCM	major merozoite su
11	42.5	57.4	1726	2 A45948	blastopia polyprot
12	42	56.8	1333	2 S38635	Ig heavy chain V-D
13	41	55.4	123	2 G48677	siderophore/surfac
14	41	55.4	447	2 H97146	hypothetical prote
15	41	55.4	899	2 G36812	class II histocomp
16	40.5	54.7	245	2 S29980	hypothetical prote
17	40	54.1	79	2 D85794	lacyl-carrier-prot
18	40	54.1	194	2 G64026	oligopeptidase (EC
19	40	54.1	601	1 A55485	oligopeptidase
20	40	54.1	601	2 G86840	hypothetical prote
21	40	54.1	644	2 S46746	Ig heavy chain V r
22	39	52.7	102	2 PH1491	Ig heavy chain V r
23	39	52.7	119	2 PH1516	Ig heavy chain V r
24	39	52.7	119	2 PH1518	Ig heavy chain V r
25	39	52.7	119	2 PH1519	Ig heavy chain V-D
26	39	52.7	123	2 F48677	Ig heavy chain V r
27	39	52.7	135	2 PH1494	Ig heavy chain V r
28	39	52.7	140	2 PH1488	Ig heavy chain V r
29	39	52.7	189	2 G97978	conserved hypothet

adenylate kinase (type II restrictio  
probable acetyl-Co  
type IIS restricti  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
trNA-pseudouridine  
probable hexosyltr  
hypothetical prote  
endo-1,4-beta gluc  
cellulase (EC 3.2.  
methyl-accepting c  
hemagglutinin-neur

## ALIGNMENTS

### RESULT 1

BTCLTN tentoxylisin (EC 3.4.24.68) precursor - Clostridium tetani

N; Alternate names: tetanus neurotoxin

C; Species: Clostridium tetani

C; Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 18-Jun-1999

C; Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364

R; Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel

EMBO J. 5, 2495-2502, 1986

A; Title: Tetanus toxin: primary structure, expression in E. coli, and homology with

A; Reference number: A25689; MUID:87053814

A; Accession: A25689

A; Molecule type: DNA

A; Residues: 1-1315 <EIS>

A; Cross-references: GB:X04436; NID:940769; PIDN:CAA28033.1; PID:940770

R; Fairweather, N.F.; Lyness, V.A.

Nucleic Acids Res. 14, 7809-7812, 1986

A; Title: The complete nucleotide sequence of tetanus toxin.

A; Reference number: A25757; MUID:87040747

A; Accession: A25757

A; Molecule type: DNA

A; Residues: 1-1315 <FAI>

A; Cross-references: GB:X06214; NID:940773; PIDN:CAA29564.1; PID:940774

A; Experimental source: strain CN3911

R; Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.

J. Bacteriol. 163, 21-27, 1986

A; Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C

A; Reference number: A25194; MUID:86085672

A; Accession: A25194

A; Molecule type: DNA

A; Residues: 743-1315 <FA2>

A; Cross-references: GB:M12739; NID:9144920; PIDN:AAA23282.1; PID:9144921

A; Accession: B25194

A; Molecule type: protein

A; Residues: 865-894 <FA3>

R; Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.

Infect. Immun. 57, 3588-3593, 1989

A; Title: Isolation, purification, and characterization of fragment B, the NH-2-termi

A; Reference number: A60759; MUID:90035436

A; Accession: A60759

A; Molecule type: protein

A; Residues: 461-475 <MA2>

R; Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Wildmann, C.; Corradin, G.

J. Immunol. 142, 394-402, 1989

A; Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.

A; Reference number: JS0098; MUID:89093918

A; Contents: annotation; epitope region

R; Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta,

Nature 359, 832-835, 1992

A; Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by prote

A; Reference number: S27125; MUID:93063293

A; Contents: annotation

R:de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.  
Eur. J. Biochem. 229, 61-69, 1995

A:Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.  
A:Reference number: S69348; MUID:95262688

A:Accession: S69348

A:Molecule type: protein

A:Residues: 2-31 <DEF>

C:Comment: The source of this protein was an extrachromosomal plasmid.

C:Comment: The precursor is cleaved by endogenous proteinase activity to form light (fra

g) and heavy (frag) chains. The amino end of the heavy chain (fragment B) is

internalized in a lipid bilayer. Fragment C binds to ganglionic

acetylcholine receptors. This potent neurotoxin binds to peripheral neuronal synapses, is internalized

and inhibits neurotransmitter release by proteolytic cleavage of synaptic

vesicles.

C:Function: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt

osomal protein.

C:Keywords: tetanus toxin

C:Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc

F:2-457/Product: tentoxylisin light chain (fragment A) #status predicted <TTL>

F:461-1315/Product: tentoxylisin heavy chain (fragment B.C) #status experimental <TTH>

F:461-864/Domains: channel forming (fragment B) #status predicted <TXB>

F:865-1315/Domains: ganglioside binding (fragment C) #status predicted <TXC>

F:233,237/Binding site: zinc (His) #status predicted

F:234/Active site: Glu #status predicted

Query Match 100.0%; Score 74; DB 1; Length 1315;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

DB 830 QYIKANSKFIGITEL 844

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A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992

C:Genetics:

A:Gene: 84

A:Start codon: GTG

Query Match 59.5%; Score 44; DB 2; Length 66;

Best Local Similarity 57.1%; Pred. No. 0.58;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YIKANSKFIGITEL 15

DB 50 YIKRNGKFGVTWEV 63

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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 : Search time 84.9789 Seconds  
(without alignments)  
414.343 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEMG.....LLDPDQDQYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

arched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

1:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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7:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1685	100.0	317	19 AAW83195	Human osteoprotegerin
2	1685	100.0	317	19 AAW69957	NF-kB receptor act
3	1685	100.0	317	19 AAW68293	NF-kB receptor act
4	1685	100.0	317	21 AAY84417	Amino acid sequenc
5	1685	100.0	317	22 AAE08738	Human receptor act
6	1685	100.0	317	22 AAE04426	Human receptor act
7	1685	100.0	317	22 AAE01993	Human full-length
8	1677	99.5	317	19 AAW83018	Osteoclastogenesis
9	1417.5	84.1	316	19 AAW83194	Human osteoprotege
10	1417.5	84.1	316	19 AAW83017	Osteoclastogenesis
11	1417.5	84.1	316	19 AAW59654	Amino acid sequenc

12	1417.5	84.1	316	20 AAY17874	Murine TRANCE. Mu
13	1417.5	84.1	316	21 AAY91024	Mouse OBM protein
14	1417.5	84.1	316	21 AAY84418	Amino acid sequenc
15	1417.5	84.1	316	21 AAY84419	Amino acid sequenc
16	1396.5	82.9	318	22 AAB82092	Rat osteoclast dif
17	1326.5	78.7	294	19 AAW69956	NF-kB receptor act
18	1326.5	78.7	294	19 AAW68292	NF-kB receptor act
19	1326.5	78.7	294	22 AAE08737	Murine receptor ac
20	1326.5	78.7	294	22 AAE04425	Murine receptor ac
21	1326.5	78.7	294	22 AAE01992	Murine RANKL (rece
22	1294	76.8	246	19 AAW83020	Osteoclastogenesis
23	1293	76.7	245	20 AAY17873	Human TRANCE. Hom
24	1136	67.4	501	22 AAB84420	Amino acid sequenc
25	1109	65.8	244	19 AAW83019	A murine OCIF-bind
26	852	50.6	160	21 AAB08273	Amino acid sequenc
27	814	48.3	152	22 AAB67248	Human RANKL. Homo
28	790	46.9	170	22 AAU08386	Mouse FLAG-murine
29	771	45.8	187	21 AAY84420	Amino acid sequenc
30	769	45.6	173	21 AAY84421	Amino acid sequenc
31	768	45.6	160	21 AAB08272	Amino acid sequenc
32	759	45.0	173	21 AAY84422	A murine osteoprot
33	721.5	42.8	188	21 AAY84423	An osteoprotegerin
34	711.5	42.2	182	21 AAY84424	An osteoprotegerin
35	691	41.0	173	21 AAY84425	DNA encoding osteo
36	683	40.5	139	21 AAY91023	Mouse OBM protein
37	670	39.8	173	21 AAY84426	An osteoprotegerin
38	317.5	18.8	74	21 AAY91020	Mouse OBM protein
39	252.5	15.0	281	20 AAY27016	Human Apo-2 ligand
40	252.5	15.0	281	20 AAY27017	Human Apo-2 ligand
41	251.5	14.9	279	19 AAW76332	Human TL2 (TRAIL),
42	251.5	14.9	279	20 AAW95032	Tumour necrosis fa
43	251.5	14.9	281	18 AAW27134	Human Apoptosis in
44	251.5	14.9	281	18 AAW19787	Human Apoptosis in
45	251.5	14.9	281	18 AAW19777	Novel cytokine Apo

ALIGNMENTS

RESULT 1  
AAW83195

ID AAW83195 standard; Protein; 317 AA.

XX AAW83195;

DT 11-FEB-1999 (first entry)

Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.  
Human: osteoprotegerin binding protein; OPG binding protein; arthritis;  
osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;  
hypercalcaemia; osteoclast differentiation and activation receptor;  
Paget's disease.

OS Homo sapiens.

PN WO9846751-A1.

PD 22-OCT-1998.

XX 15-APR-1998; 98WO-US07584.

XX 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

PA (AMGE-) AMGEN INC.

XX Boyle WJ;

XX WPI; 1998-594578/50.

DR N-PSDB; AAV70285.

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,  
 PT e.g. treating bone diseases by modulating osteoclast differentiation  
 PT and for diagnosis

PS Claim 19; Fig 4; 47pp; English.

XX The present sequence is human osteoprotegerin (OPG) binding protein.  
 CC Host cells transfected with vectors containing nucleic acid molecules  
 CC encoding OPG binding protein are used to produce recombinant OPG binding  
 CC protein. OPG binding protein is used in binding assays to determine  
 CC osteoprotegerin (OPG) in biological samples; to screen for specific  
 CC binding agents (particularly agonists and antagonists, including  
 CC intracellular proteins); to raise Ab (useful in immunoassays for  
 CC detection of OPG binding protein) and to identify compounds that  
 CC modulate binding of OPG binding protein to osteoclast differentiation  
 CC and activation receptor (OAR). The nucleic acid molecule encoding OPG  
 CC binding protein can be used to detect OPG binding protein-encoding  
 CC sequences, e.g. screening for related sequences, also to produce  
 CC transgenic animal models, while complementary sequences are used for  
 CC antisense regulation of OPG binding protein expression. Modulators of  
 CC OPG binding protein, particularly soluble forms of OPG binding protein  
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,  
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's  
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,  
 CC optionally in combination with agents that promote bone growth.

XX Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 19; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEMGCGPAPHEGPHAPPAPPPAPPPAPPAASRMFVALLGLGQV 60  
 DB 1 MRRASRDYTKYLRGSEMGCGPAPHEGPHAPPAPPPAPPPAPPAASRMFVALLGLGQV 60  
 QY 61 VCSVALFFYFRQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 DB 61 VCSVALFFYFRQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 QY 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPPAHLINATDIPSGSH 180  
 DB 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPPAHLINATDIPSGSH 180  
 QY 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 DB 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWNSGFHFYSINVGFFKLRSGEISIEVSNPSLLD 300  
 DB 241 YVTKTSIKIPSSHTLMKGGSTKYWNSGFHFYSINVGFFKLRSGEISIEVSNPSLLD 300  
 QY 301 PQDATYFGAFKVRDID 317  
 DB 301 PQDATYFGAFKVRDID 317

RESULT 2

AAW69957  
 ID AAW69957 standard; Protein; 317 AA.

XX AC

XX AAW69957;

XX DT 08-OCT-1998 (first entry)

XX DE NF-kB receptor activator RANK ligand (RANKL).

XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
 KW immune response; inflammatory response; toxic shock; sepsis;  
 KW RANKL; RANK ligand; tumour necrosis factor; TNF.

XX OS Homo sapiens.

XX

PN WO9828426-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23775.

XX PR 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX PR 07-MAR-1997; 97US-0813509.

XX PA (IMV) IMMUNEX CORP.

XX PI Anderson DM, Galibert LJ, Maraskovsky E;

XX DR WPI: 1998-377657/32.

XX DR N-PSDB; AAV41378.

XX PT New isolated ligand for receptor activator of NF-kappa B - used to  
 PT develop products for augmenting an immune response for inhibiting an  
 PT inflammatory response and for protection of cells

XX PS Claim 27; Pages 59-60; 80pp; English.

XX This represents a human RANKL, a ligand for the RANK (receptor  
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a  
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK  
 CC may be used for inhibiting activation of NF-kB, by contacting a cell  
 CC expressing membrane-associated RANK with a soluble RANK which binds to  
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be  
 CC used to induce maturation of dendritic cells and enhance their  
 CC allo-stimulatory capacity, thereby augmenting an immune response. The  
 CC soluble RANK polypeptide composition may also be used for regulating an  
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists  
 CC may be useful in ameliorating negative effects of an inflammatory  
 CC response that result from triggering of RANK, e.g. in treating toxic  
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory  
 CC reactions. They can also be used in adjunct therapy for disease  
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides  
 CC can also be used to identify inhibitors of RANK and thus inhibitors of  
 CC an inflammatory response, and also for protecting RANK-expressing cells  
 CC from the negative effects of chemotherapy or the presence of high levels  
 CC of TNF-alpha. The products can also be used for detection and drug  
 CC screening.

XX SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 19; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEMGCGPAPHEGPHAPPAPPPAPPPAPPAASRMFVALLGLGQV 60  
 DB 1 MRRASRDYTKYLRGSEMGCGPAPHEGPHAPPAPPPAPPPAPPAASRMFVALLGLGQV 60  
 QY 61 VCSVALFFYFRQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 DB 61 VCSVALFFYFRQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 QY 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPPAHLINATDIPSGSH 180  
 DB 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPPAHLINATDIPSGSH 180  
 QY 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 DB 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWNSGFHFYSINVGFFKLRSGEISIEVSNPSLLD 300  
 DB 241 YVTKTSIKIPSSHTLMKGGSTKYWNSGFHFYSINVGFFKLRSGEISIEVSNPSLLD 300  
 QY 301 PQDATYFGAFKVRDID 317  
 DB 301 PQDATYFGAFKVRDID 317

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XX The present sequence represents a human osteoprotegerin ligand (OPGL).  
CC Osteoprotegerin is a secreted member of the tumour necrosis factor  
CC receptor family, which blocks osteoclastogenesis in a dose dependent  
CC manner. The OPGL protein is synthesised as a type II transmembrane  
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL  
CC is a potent osteoclast differentiation factor when combined with CSF-1  
CC It is not capable of inducing osteoclast differentiation in the absence  
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The  
CC specification describes a method for the *in vivo* down-regulation of  
CC OPGL activity in an animal. The method comprises using at least one OPGL  
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce  
CC an immune response in the animal. The method and OPGL polypeptide are

CC useful for treating, preventing and ameliorating osteoporosis or other  
CC diseases or conditions characterised by excessive bone resorption.

1

SQ	Sequence	317	AA;
Query Match	100.0%	Score 1685;	DB 21; Length 317;
Best Local Similarity	100.0%	Pred. No. 2.6e-156;	
Matches 317;	Conservative	0;	Mismatches 0; Indels 0; Caps 0;

QY	1	MRASDVTYKYLRGSEEMGGPCADHEGPHLHAPPAPHOPPAARSMFVALLGLGQV	60
Db	1	MRASDVTYKYLRGSEEMGGPCADHEGPHLHAPPAPHOPPAARSMFVALLGLGQV	60
QY	61	VCSVALFFYFRAQMPNRISEDTGTHCIYRILRLHENADFQDTLLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMPNRISEDTGTHCIYRILRLHENADFQDTLLESQDTKLIPDSCRRIK	120
QY	121	QAFQAGAVQELQHIYVGSQHIRAEKAMVDSWLDLAKRSKLEAQPHAHLTINATDIPSGSH	180
Db	121	QAFQAGAVQELQHIYVGSQHIRAEKAMVDSWLDLAKRSKLEAQPHAHLTINATDIPSGSH	180
QY	181	KVSLSWYHDRGWAKISNNMTFSGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLM	240
Db	181	KVSLSWYHDRGWAKISNNMTFSGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLM	240
QY	241	YVTKTSIKIPSSHTLMKGSTKYWCNSNFEHYISINVGGFFKLRCSEETISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGSTKYWCNSNFEHYISINVGGFFKLRCSEETISIEVSNPSLLD	300
QY	301	POODATYFGAFKVRDID	317
Db	301	POODATYFGAFKVRDID	317

RESULT 5  
AAE08738  
ID AAE08738 standard; Protein; 317 AA.

AC AAE08738;

15-NOV-2001 (first entry)

Human receptor activator of NF kappaB ligand (RANKL) protein.

Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

*Homo sapiens.*

PN 1 US6271349-B1.

XX  
PD  
07-AUG-2001

XX 17-DEC-1998: 98US-0215649.

XX  
PR 23-DEC-1996: 96US-0059978.

PR 07-MAR-1997; 970S-0077181.  
PR 14-OCT-1997; 970S-0064671

PR 23-DEC-1996; 96US-0772330.  
PR 07-MAR-1997; 97US-0813509

PR 22-DEC-1997; 97US-0996139.  
yy

PA (IMMV) IMMUNEX CORP.

PI Dougall WC, Galibert L;

DR WPI; 2001-520313/57.

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**PT** New receptor activator of NF-kappaB (RANK) polypeptides, useful for

Id  
Id  
Id

XX  
PS Example 15: Col

Example 15: Column 71-72; 47pp; English.

The patent discloses novel receptor activator of nuclear factor (NF)-kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of the tumour necrosis factor (TNF) receptor superfamily and associates with TNF receptor associated factor (TRAF) 2 and 3 which are important in the regulation of immune and inflammatory response. The receptors are useful for regulating immune response and in screening for inhibitors of these receptors. The cytoplasmic domain of RANK is used in developing assays for inhibitors of signal transduction, e.g. for screening the molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful in ameliorating the negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory reactions and the effects of bone resorption. RANK acts as an anti-apoptotic signal and rescue the cells that express RANK from apoptosis. Soluble forms of the receptor are used in vivo or in vitro based screening tests for agonists or antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B activation, or to inhibit transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast precursors and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is RANK ligand (RANKL) protein from human.

Sequence	317 AA;
SQ	

Query Match	100.0%	Score 1685;	DB 22;	Length 317;
Best Local Similarity	100.0%;	Pred. No. 2.6e-156;		
Matches 317;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0			

0v 1 MRRASRDYTKYLRGSEEMGGPGAPHEGCLHAPPPAPHOPPAASRSMEVALIGLGLGOV 60

db 1 MRRASRDYTKYLRGSEEMGGPGAPHEGPLHAPPPAPHOPPPAASRSMFVALIGLIGOV 60

61 VCSVALEEFYERAOBPNRISEDGTHCTYRTLRHENADEODTLESODTKLIPDSCRRIK 120

61 VCSVAIEEVEPRAOMDPRISEDCETHCIYRIIRIHENADEODTLESODTKIIPDSCBRIK 120

121 08E0CAV06E10HTVCSOUTRBEKAMTCSWI DI AKPSKI EAPDEAHITINATDTPSCSH 180

121 08E0CAV06E1 08TVCS041918AFKAMUTCSTW DI AYPSKI F8APBEAHI TINATIDPSSCY 180

101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 109

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

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[illegible][illegible]

## RESULT 6

AAE04426

ID AAE04426 standard; Protein; 317 AA.

XX







DR WPI; 1998-594578/50.  
 DR N-PSDB; AAV70284.  
 XX Nucleic acid encoding osteoprotegerin binding protein - useful for,  
 PT e.g. treating bone diseases by modulating osteoclast differentiation  
 PT and for diagnosis  
 XX  
 XX Claim 19; Fig 1; 47pp; English.  
 XX  
 XX The present sequence is human osteoprotegerin (OPG) binding protein.  
 CC Host cells transfected with vectors containing nucleic acid molecules  
 CC encoding OPG binding protein are used to produce recombinant OPG binding  
 CC protein. OPG binding protein is used in binding assays to determine  
 CC osteoprotegerin (OG) in biological samples; to screen for specific  
 CC binding agents (particularly agonists and antagonists, including  
 CC intracellular proteins); to raise Ab (useful in immunoassays for  
 CC detection of OPG binding protein) and to identify compounds that  
 CC modulate binding of OPG binding protein to osteoclast differentiation  
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG  
 CC binding protein can be used to detect OPG binding protein-encoding  
 CC sequences, e.g. screening for related sequences, also to produce  
 CC transgenic animal models, while complementary sequences are used for  
 CC antisense regulation of OPG binding protein expression. Modulators of  
 CC OPG binding protein, particularly soluble forms of OPG binding protein  
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,  
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's  
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,  
 CC optionally in combination with agents that promote bone growth.  
 XX  
 XX Sequence 316 AA;

Query Match 84.1%; Score 1417.5; DB 19; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
 QY 1 MRRASRDYTKYLRSGEMGGPCAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 59  
 DB 1 MRRASRDYTKYLRSGEMGGPCVPHGPHLPAPAPAPPAPPAASRSMFVALLGLGQ 60  
 QY 60 VVCSVALFFYFRAQMDPNRISEDTGHCYIRILRHENADFDQTTLESQDTKLIPDSCRRI 119  
 DB 61 VVCSIALFLYFRAQMDPNRISEDTGHCYIRILRHENAGLDSTLESDT--LPDSCRM 118  
 QY 120 KQAFQAVQKELQHVGSQHIRAEKAWDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179  
 DB 119 KQAFQAVQKELQHVGPQRFSGAPAMMGSGWLDVAQRKPEAQPFAHLTINAAIPSGS 178  
 QY 240 VVYTKTSIKIPSSHTLMKGGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VVYTKTSIKIPSSHNLKMGSTKYNSGSEFHFYSINVGFFKLRAGEEISIQVSNPSLL 298  
 QY 300 DPQDATYFGAFKVRDID 317  
 DB 299 DPQDATYFGAFKVRQDID 316

RESULT 10  
 AAW83017  
 ID AAW83017 standard; Protein; 316 AA.  
 XX  
 AC AAW83017;  
 XX  
 DT 10-FEB-1999 (first entry)  
 XX Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).  
 DE Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;  
 KW Osteoclast; bone absorption factor; bone disorder; calcium metabolism.  
 XX

OS Unidentified.  
 FN W09846644-AI.  
 XX  
 XX 22-OCT-1998.  
 PD  
 XX  
 XX 15-APR-1998; 98WO-JP01728.  
 PF  
 XX  
 XX 02-DEC-1997; 97JP-0332241.  
 PR  
 XX 15-APR-1997; 97JP-0097808.  
 PR  
 XX 09-JUN-1997; 97JP-0151434.  
 PR  
 XX 12-AUG-1997; 97JP-0217897.  
 PR  
 XX 21-AUG-1997; 97JP-0224803.  
 XX  
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.  
 PA  
 XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;  
 XX Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;  
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;  
 PI  
 XX WPI; 1998-594563/50.  
 DR N-PSDB; AAV69886.  
 DR  
 XX Protein binding to osteoclastogenesis inhibitory factor - useful  
 PT for, e.g. treatment and investigation of disorders of bone and  
 PT calcium metabolism  
 XX  
 XX Claim 8; Pages 106-108; 151pp; Japanese.  
 PS  
 XX The present sequence represents an osteoclastogenesis inhibitory factor  
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the  
 CC separation and maturation of osteoclasts in the presence of bone  
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).  
 CC OBM is isolated from stroma cells cultured in the presence of a bone  
 CC absorption factor by separation and solubilisation of membrane proteins  
 CC then affinity chromatography using OCIF. It exists in a full-sequence  
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be  
 CC used for screening potential inhibitors and modifiers of its biological  
 CC activity, and screening for receptors to OBM which mediate its function.  
 CC These substances can then be used in the treatment of disorders of bone  
 CC function and calcium metabolism. The antibodies can be used for assay  
 CC of the protein, for investigative and diagnostic purposes, and as  
 CC components of drugs.  
 XX  
 XX Sequence 316 AA;

Query Match 84.1%; Score 1417.5; DB 19; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
 QY 1 MRRASRDYTKYLRSGEMGGPCAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 59  
 DB 1 MRRASRDYTKYLRSGEMGGPCVPHGPHLPAPAPAPPAPPAASRSMFVALLGLGQ 60  
 QY 60 VVCSVALFFYFRAQMDPNRISEDTGHCYIRILRHENADFDQTTLESQDTKLIPDSCRRI 119  
 DB 61 VVCSIALFLYFRAQMDPNRISEDTGHCYIRILRHENAGLDSTLESDT--LPDSCRM 118  
 QY 120 KQAFQAVQKELQHVGSQHIRAEKAWDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179  
 DB 119 KQAFQAVQKELQHVGPQRFSGAPAMMGSGWLDVAQRKPEAQPFAHLTINAAIPSGS 178  
 QY 180 HKVLSSTWYHDSRWAKISNNTFSGKLYNODGFYLYANICFRHETSGDLATYLQLM 239  
 DB 179 HKVLSSTWYHDSRWAKISNNTFSGKLYNODGFYLYANICFRHETSGVPTDYLQLM 238  
 QY 240 VVYTKTSIKIPSSHTLMKGGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VVYTKTSIKIPSSHNLKMGSTKYNSGSEFHFYSINVGFFKLRAGEEISIQVSNPSLL 298  
 QY 300 DPQDATYFGAFKVRDID 317  
 DB 299 DPQDATYFGAFKVRQDID 316



Query Match 84.1%; Score 1417.5; DB 20; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

CC of osteoclast in the co-culture of mouse osteoblast-like stroma cell and  
 CC mouse spleen cell in the presence of a bone absorption promoting factor  
 CC such as active type vitamin D3 and parathyroid hormone (PTH). The protein  
 CC can be used as a drug and a research reagent. The present sequence  
 CC represents a mouse OCIF binding molecule (OBM) from the present  
 CC invention.

CC  
 XX  
 SQ Sequence 316 AA;

Query Match 84.1%; Score 1417.5; DB 21; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSMFVALLGLGLGQ 59  
 DB 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSMFVALLGLGLGQ 60

QY 60 VVCSVALFFYFRAQMDPNRISDGTCHYRIIRLHENADFOPTTLESQTKLIPDSRR 119  
 DB 61 VVCSIALFLYFRAQMDPNRISDGTCHYRIIRLHENAGLDSTLESDT--LPDSRRM 118

QY 120 KQAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLLINATDIPSGS 179  
 DB 119 KQAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLLINATDIPSGS 178

QY 180 HKVLSSTWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLM 239  
 DB 179 HKVLSSTWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGSVPTDYQLM 238

QY 240 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 298

QY 300 DPQDQATYFAGKVRDID 317  
 DB 299 DPQDQATYFAGKVRDID 316

RESULT 14  
 AAY84418  
 ID AAY84418 standard; Protein; 316 AA.  
 AC AAY84418;  
 DT 25-JUL-2000 (first entry)  
 DE Amino acid sequence of a murine osteoprotegerin ligand (OPGL).  
 KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;  
 KW tumour necrosis factor receptor; type II transmembrane protein;  
 KW osteoclast differentiation; CSF-1; osteoclast activator;  
 KW immune response; osteoporosis; bone resorption.  
 XX Mus musculus.  
 OS  
 FH Key  
 FT Domain  
 FT Domain  
 FT Domain  
 FT Domain  
 FT Region  
 FT  
 XX WO200015807-A1.  
 XX  
 XX 23-MAR-2000.  
 XX 13-SEP-1999;  
 XX 15-SEP-1998;  
 XX 02-OCT-1998;

Location/Qualifiers  
 48..71  
 /note= "transmembrane domain"  
 70..157  
 /note= "extracellular stalk domain"  
 152..316  
 /note= "tumour necrosis factor-like domain"  
 158..317  
 /note= "active ligand moiety"

Query Match 84.1%; Score 1417.5; DB 20; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

CC of osteoclast in the co-culture of mouse osteoblast-like stroma cell and  
 CC mouse spleen cell in the presence of a bone absorption promoting factor  
 CC such as active type vitamin D3 and parathyroid hormone (PTH). The protein  
 CC can be used as a drug and a research reagent. The present sequence  
 CC represents a mouse OCIF binding molecule (OBM) from the present  
 CC invention.

CC  
 XX  
 SQ Sequence 316 AA;

Query Match 84.1%; Score 1417.5; DB 21; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSMFVALLGLGLGQ 59  
 DB 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSMFVALLGLGLGQ 60

QY 60 VVCSVALFFYFRAQMDPNRISDGTCHYRIIRLHENADFOPTTLESQTKLIPDSRR 119  
 DB 61 VVCSIALFLYFRAQMDPNRISDGTCHYRIIRLHENAGLDSTLESDT--LPDSRRM 118

QY 120 KQAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLLINATDIPSGS 179  
 DB 119 KQAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLLINATDIPSGS 178

QY 180 HKVLSSTWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLM 239  
 DB 179 HKVLSSTWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGSVPTDYQLM 238

QY 240 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 298

QY 300 DPQDQATYFAGKVRDID 317  
 DB 299 DPQDQATYFAGKVRDID 316

RESULT 13  
 AAY91024  
 ID AAY91024 standard; Protein; 316 AA.  
 AC AAY91024;  
 DT 05-SEP-2000 (first entry)  
 DE Mouse OBM protein sequence SEQ ID NO:10.  
 KW Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF;  
 KW OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH;  
 KW parathyroid hormone.  
 XX Mus sp.  
 OS  
 JP2000102390-A.  
 PD 11-APR-2000.  
 PF 30-SEP-1998; 98JP-0292971.  
 PR 30-SEP-1998; 98JP-0292971.  
 XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 PA (YSNE-) YS NEW TECHNOLOGY KENKYUSHO.  
 XX  
 DR WPI; 2000-332087/29.  
 DR N-PSDB; AAA39156.  
 XX  
 PT A DNA and preparation of a protein by using it  
 XX  
 PS Example 1; Page 15-16; 18pp; Japanese.  
 CC The present invention describes a genomic DNA encoding a protein having  
 CC an activity of supporting or promoting differentiation and maturation of  
 CC osteoclasts. The genomic DNA encoding a protein has the following  
 CC properties: (a) combines specifically with osteoclastogenesis inhibitory  
 CC factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)  
 CC of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide  
 CC gel electrophoresis) under a nonreductive condition and the apparent mw  
 CC when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c)  
 CC has an activity of supporting or promoting differentiation and maturation

XX PA (MEBI-) M & E BIOTECH AS.  
 XX PI Halkier T, Haaning J;  
 XX WPI; 2000-271444/23.  
 DR N-PSDB; AA299965.  
 XX  
 XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used  
 PT to treat, prevent and ameliorate osteoporosis -  
 XX  
 XX Claim 17; Page 81-82; 110pp; English.  
 XX  
 XX The present sequence represents a murine osteoprotegerin ligand (OPGL).  
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor  
 CC receptor family, which blocks osteoclastogenesis in a dose dependent  
 CC manner. The OPGL protein is synthesised as a type II transmembrane  
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL  
 CC is a potent osteoclast differentiation factor when combined with CSF-1.  
 CC It is not capable of inducing osteoclast differentiation in the absence  
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The  
 CC specification describes a method for the in vivo down-regulation of  
 CC OPGL activity in an animal. The method comprises using at least one OPGL  
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce  
 CC an immune response in the animal. The method and OPGL polypeptide are  
 CC useful for treating, preventing and ameliorating osteoporosis or other  
 CC diseases or conditions characterised by excessive bone resorption.  
 XX  
 XX SQ Sequence 316 AA;  
 XX  
 XX Query Match 84.1%; Score 1417.5; DB 21; Length 316;  
 XX Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 XX Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
 QY 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPHAPHPAPPAASRSMFVALLGLGLGQ 59  
 DB 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPHAPHPAPPAASRSMFVALLGLGLGQ 60  
 QY 60 VVCSVALFFYFRAQMDPNRISEDTCHCYRILRLHENAADFDTTLESODTKLIPDSCRR 119  
 DB 61 VVCSIALFLYFRAQMDPNRISEDTCHCYRILRLHENAADFDTTLESODTKLIPDSCRR 118  
 QY 120 KQAFQAVQKELQHVGSQHTIRAEKAMVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179  
 DB 119 KQAFQAVQKELQHVGSQHTIRAEKAMVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 178  
 QY 180 HKVLSWYHNRGWAKISNMFTSGNKLIVNODGGFYLYANICFRHHETSGVPTDYQLM 239  
 DB 179 HKVTLSSWYHNRGWAKISNMFTSGNKLIVNODGGFYLYANICFRHHETSGVPTDYQLM 238  
 QY 240 VYVTKTSIKIPSSHTLMKGGSTKYVNSGSEPHFYSINVGFFKLRSGEISIEVSNPSSL 299  
 DB 239 VYVTKTSIKIPSSHTLMKGGSTKYVNSGSEPHFYSINVGFFKLRSGEISIEVSNPSSL 298  
 QY 300 DPQDQATYFGAFKVRDID 317  
 DB 299 DPQDQATYFGAFKVRDID 316  
 RESULT 15  
 ID AAY84419  
 AC AAY84419 standard; Protein; 316 AA.  
 XX  
 XX Amino acid sequence of a murine osteoprotegerin ligand (OPGL).  
 DT  
 XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;  
 KW tumour necrosis factor receptor; type II transmembrane protein;  
 KW osteoclast differentiation; CSF-1; osteoclast activator;  
 KW immune response; osteoporosis; bone resorption.

XX OS Mus musculus.  
 XX FH Key Location/Qualifiers  
 FT Region 49..69 /note= "transmembrane region"  
 FT Domain 70..157 /note= "extracellular stalk domain"  
 FT Region 158..317 /note= "active ligand moiety"  
 XX W0200015807-A1.  
 XX 23-MAR-2000.  
 XX 13-SEP-1999; 99WO-DK00481.  
 XX 15-SEP-1998; 98DK-0001164.  
 PR 02-OCT-1998; 98US-0102896.  
 XX (MEBI-) M & E BIOTECH AS.  
 XX Halkier T, Haaning J;  
 WPI; 2000-271444/23.  
 DR N-PSDB; AA299966.  
 XX  
 XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used  
 PT to treat, prevent and ameliorate osteoporosis -  
 XX  
 XX Claim 17; Page 85-86; 110pp; English.  
 XX  
 XX The present sequence represents a murine osteoprotegerin ligand (OPGL).  
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor  
 CC receptor family, which blocks osteoclastogenesis in a dose dependent  
 CC manner. The OPGL protein is synthesised as a type II transmembrane  
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL  
 CC is a potent osteoclast differentiation factor when combined with CSF-1.  
 CC It is not capable of inducing osteoclast differentiation in the absence  
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The  
 CC specification describes a method for the in vivo down-regulation of  
 CC OPGL activity in an animal. The method comprises using at least one OPGL  
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce  
 CC an immune response in the animal. The method and OPGL polypeptide are  
 CC useful for treating, preventing and ameliorating osteoporosis or other  
 CC diseases or conditions characterised by excessive bone resorption.  
 XX  
 XX SQ Sequence 316 AA;  
 XX  
 XX Query Match 84.1%; Score 1417.5; DB 21; Length 316;  
 XX Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 XX Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
 QY 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPHAPHPAPPAASRSMFVALLGLGLGQ 59  
 DB 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPHAPHPAPPAASRSMFVALLGLGLGQ 60  
 QY 60 VVCSVALFFYFRAQMDPNRISEDTCHCYRILRLHENAADFDTTLESODTKLIPDSCRR 119  
 DB 61 VVCSIALFLYFRAQMDPNRISEDTCHCYRILRLHENAADFDTTLESODTKLIPDSCRR 118  
 QY 120 KQAFQAVQKELQHVGSQHTIRAEKAMVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179  
 DB 119 KQAFQAVQKELQHVGSQHTIRAEKAMVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 178  
 QY 180 HKVLSWYHNRGWAKISNMFTSGNKLIVNODGGFYLYANICFRHHETSGVPTDYQLM 239  
 DB 179 HKVTLSSWYHNRGWAKISNMFTSGNKLIVNODGGFYLYANICFRHHETSGVPTDYQLM 238  
 QY 240 VYVTKTSIKIPSSHTLMKGGSTKYVNSGSEPHFYSINVGFFKLRSGEISIEVSNPSSL 299  
 DB 239 VYVTKTSIKIPSSHTLMKGGSTKYVNSGSEPHFYSINVGFFKLRSGEISIEVSNPSSL 298



Qy 300 DPQDATYFGAKVRDID 317  
|||||  
Db 299 DPQDATYFGAKVQDID 316

Search completed: October 10, 2002, 16:00:55  
Job time : 88.9789 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 37.2379 seconds  
(without alignments)  
329.613 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRYTKYLRGSEMG...LLDPDQDATYGFQKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Arched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1685	100.0	317	1 TN11_HUMAN	O14788 h tumor nec
2	1417.5	84.1	316	1 TN11_MOUSE	O35235 m tumor nec
3	251.5	14.9	281	1 TN10_HUMAN	P50591 homo sapien
4	248	14.7	291	1 TN10_MOUSE	P50592 mus musculus
5	189	11.2	281	1 FASL_HUMAN	P48023 homo sapien
6	184.5	10.9	279	1 FASL_MOUSE	P41047 mus musculus
7	176.5	10.5	261	1 TNF5_BOVIN	P51749 bos taurus
8	175.5	10.4	278	1 FASL_RAT	P36940 rattus norv
9	158.5	9.4	261	1 TNF5_HUMAN	P29965 homo sapien
10	152	9.0	260	1 TNF5_FELCA	O97605 felis silve
11	146	8.7	234	1 TNFA_CANVPO	P51435 cavia porce
12	145	8.6	260	1 TNF5_CANFA	O97626 canis famill
13	141.5	8.4	235	1 TNFA_MOUSE	P06804 mus musculus
14	140.5	8.3	235	1 TNFA_RABIT	P04924 oryctolagus
15	137	8.1	234	1 TNFA_SHEEP	P23383 ovis aries
16	134	8.0	233	1 TNFA_MACEFA	P79337 macaca fasc
17	134	8.0	240	1 TN14_HUMAN	O43557 homo sapien
18	133	7.9	233	1 TNFA_CANFA	P51742 canis famill
19	133	7.9	233	1 TNFA_HUMAN	P01375 homo sapien
20	133	7.9	233	1 TNFA_MACMU	P48094 macaca mula
21	132.5	7.9	235	1 TNFA_PERLE	P36939 peromyscus
22	131.5	7.8	235	1 TNFA_RAT	P16599 rattus norv
23	130.5	7.7	306	1 TNFC_MOUSE	P41155 mus musculus
24	130	7.7	233	1 TNFA_PAPSP	P33620 papio sp. (
25	129.5	7.7	233	1 TNFA_MARMO	O35734 marmota mon
26	129	7.7	233	1 TNFA_PAPHU	O77510 papio hamad
27	128	7.6	234	1 TNFA_HORSE	P29553 equus cabal
28	126.5	7.5	233	1 TNFA_BOVIN	O06599 bos taurus
29	126	7.5	232	1 TNFA_PIG	P23563 sus scrofa
30	122	7.2	193	1 TNFA_CAPHI	P13296 capra hircu
31	120	7.1	229	1 TNFA_CEREL	P51743 cervus elap
32	118	7.0	260	1 TNF5_MOUSE	P27548 mus musculus
33	117	6.9	233	1 TNFA_FELCA	P19101 felis silve

34	117	6.9	244	1 TNFC_HUMAN	O05643 homo sapien
35	116	6.9	233	1 TNFA_MACEU	O77764 macropus eu
36	105	6.2	201	1 TNFB_MACEU	O9448 macropus eu
37	97	5.8	1464	1 CALL_HUMAN	P02452 homo sapien
38	95	5.6	858	1 V2A_CANV	O86783 cucumer mo
39	93	5.5	233	1 TNFA_TRIVU	P79374 trichosurus
40	92.5	5.5	205	1 TNFB_HUMAN	P01374 homo sapien
41	92.5	5.5	450	1 YK22_YEAST	P36135 saccharomyc
42	92	5.5	857	1 V2A_CANVT	O40977 cucumer mo
43	90.5	5.4	858	1 V2A_CANVAS	O39436 cucumer mo
44	90.5	5.4	1694	1 SN_MOUSE	O62230 mus musculus
45	90	5.3	1460	1 CALL_CANFA	O9x5j7 canis famill

## ALIGNMENTS

RESULT 1					
ID	TN11_HUMAN	STANDARD;	PRT;	317 AA.	
AC	O14788: O14723; Q9P203;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator				
DE	of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-				
DE	induced cytokine) (TNF) (Osteoprotegerin ligand) (OPGL) (Osteoclast				
DE	differentiation factor) (ODF) (OPGL).				
GN	TNFSF11 OR RANKL OR TNF OR OPGL.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Bone marrow, and Peripheral blood;				
RX	MEDLINE-98032977; PubMed-9367155;				
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,				
RA	Tcmetsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,				
RA	Galibert L.;				
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth				
RT	and dendritic-cell function.";				
RL	Nature 390:175-179(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Lymph node;				
RC	MEDLINE-98227661; PubMed-9568710;				
RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,				
RA	Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,				
RA	Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,				
RA	Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Delaney J.,				
RA	Boyle W.J.;				
RT	"Osteoprotegerin ligand is a cytokine that regulates osteoclast				
RT	differentiation and activation.";				
RL	Cell 93:165-176(1998).				
RN	[3]				
RP	SEQUENCE OF 73-317 FROM N.A.				
RC	TISSUE-Thymocytes;				
RC	MEDLINE-97460112; PubMed-9312132;				
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,				
RA	Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,				
RA	Choi Y.;				
RT	"TNF is a novel ligand of the tumor necrosis factor receptor family				
RT	that activates c-Jun N-terminal kinase in T cells.";				
RL	J. Biol. Chem. 272:25190-25194(1997).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	TISSUE-Tongue;				
RC	MEDLINE-20175237; PubMed-10708588;				
RA	Nagai M., Kyakumoto S., Sato N.;				
RA	"Cancer cells responsible for humoral hypercalcemia express mRNA				
RT	encoding a secreted form of ODF/TNFR that induces osteoclast				
RT	formation.";				

Biochem. Biophys. Res. Commun. 269:532-536(2000).  
-1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.  
AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL  
PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS  
BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE  
REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY  
AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL  
HYPERCALCEMIA OF MALIGNANCY.  
-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND  
SECRETED (ISOFORM 2).  
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE  
PRODUCED BY ALTERNATIVE SPLICING.  
-1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT  
WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,  
PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.  
-1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.  
-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
-----  
EMBL; AF019047; AAB86811.1; -  
EMBL; AF053712; AAC39731.1; -  
EMBL; AF013171; AAC51762.1; -  
EMBL; AB037599; BAA90488.1; -  
MIM; 602642; -  
InterPro: IPR003263; TNF\_5.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF; 1.  
DR ProDom: PD008600; TNF\_5; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS00251; TNF\_1; FALSE\_NEG.  
DR PROSITE: PS00049; TNF\_2; 1.  
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;  
KW Signal-anchor; Alternative splicing.  
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)  
FT DOMAIN 69 317 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 171 171 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 198 198 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT VARSPLIC 1 73 MISSING (IN ISOFORM 2).  
FT CONFLICT 194 194 A -> G (IN REF. 3).  
SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;  
  
Jury Match 100.0%; Score 1685; DB 1; Length 317;  
Best Local Similarity 100.0%; Pred. No. 7.4e-136;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRRASRDYTKYLGRSEMGPGAPHEGLHAPPAPHPAPPAASRSFVALLGLGLGV 60  
DB 1 MRRASRDYTKYLGRSEMGPGAPHEGLHAPPAPHPAPPAASRSFVALLGLGLGV 60  
  
QY 61 VCSVALFFYFRAQDMPNRISDGTGHCYIRILRLHENADFQTTLESQDTKLIPDSCKRIK 120  
DB 61 VCSVALFFYFRAQDMPNRISDGTGHCYIRILRLHENADFQTTLESQDTKLIPDSCKRIK 120  
  
QY 121 QAFGAVQKELQHVGSQIHIAEKAVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
DB 121 QAFGAVQKELQHVGSQIHIAEKAVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
  
QY 181 KVSLSWHDGKAKISNMTFSNGLIYNQDFFYLYANICFRHETSGDLATEYLQLMV 240  
DB 181 KVSLSWHDGKAKISNMTFSNGLIYNQDFFYLYANICFRHETSGDLATEYLQLMV 240  
  
QY 241 YVTKTSIKIPSSHTLMKGGSTKYSGNSEFHYFYSINVGGFYKLRSGEISIEVSNPSLLD 300  
DB 241 YVTKTSIKIPSSHTLMKGGSTKYSGNSEFHYFYSINVGGFYKLRSGEISIEVSNPSLLD 300

QY 301 PPDATYFGAFKVRDID 317  
DB 301 PPDATYFGAFKVRDID 317  
  
RESULT 2  
TNII\_MOUSE  
ID TNII\_MOUSE STANDARD; PRT; 316 AA.  
AC O35235; O35305;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)  
(OCIF).  
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hybridoma;  
RX MEDLINE=97460112; PubMed=93121132;  
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,  
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
RA Choi Y.;  
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
that activates c-Jun N-terminal kinase in T cells.";  
RL J. Biol. Chem. 272:25190-25194(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=98227661; PubMed=9568710;  
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
RA Boyle W.J.;  
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
differentiation and activation.";  
RL Cell 93:165-176(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow stroma;  
RX MEDLINE=98188248; PubMed=9520411;  
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M., Tsuda E.,  
RA Mochizuki S.-I., Tomoyasu A., Yanai K., Goto M., Murakami A., Suda T.;  
RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
RT "Osteoclast differentiation factor is a ligand for  
osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
to TRANCE/RANKL.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thymic lymphoma;  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubs R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
and dendritic-cell function.";  
RL Nature 390:175-179(1997).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
IKeda T.;  
RL Submitter: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.  
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL  
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS



```
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR00478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.
DR Cytokine; Transmembrane; Signal-anchor; Apoptosis; 3D-structure.
KW DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;

Query Match 14.9%; Score 251.5; DB 1; Length 281;
Best Local Similarity 24.1%; Pred. No. 3.7e-14;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY 42 PAASRMFVALLGLGQVVCVALFFYFRAQMD--PNRISEDTGHCIVRIILRLHENADF 99
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
10 PSLGQTCVLIVFTVLQSLCAVAVTYVTNELKQMDKYKSGIACF-----LKED--- 61

QY 100 QDTLESQDTKLIPDSRRIRKQAFQAVQKQELQIYVSGHRAEKAMVDGSLDLAKRSK 159
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 62 -DSYDPNDEESMNSPCQVKW-----QLRQLVRKMLITSEETI-----STVQEQ 107

QY 160 LEAQP-----AHLT-----INATDIPSGSHKVL-----SSWYHDR-GWAKISM 199
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 108 QNISPLVRERGPORVAHITGRGNTLSSPSNKEKALGRKINSWESSRSGHSLSNL 167

QY 200 TFSNGKLIVNODGFYLYANICPRRHETSGDLATEYLQLMLVYVTKSIKIPSSHTLMKG 259
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 168 HLRGELVILHEKGYIYISQTYFRFQEEKNTKNDQKQWQYIYKVT-SYPDPILLMKSA 226

QY 260 STKYSGNSEFFHYSINVGFFKLRGEEISIEVSNPLDPPQDATYFGAFKV 313
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 227 BNSCWSKDAEYGLYISQGIPELKENDRIFSVSVTNEHLIDMDHEASFFGAFLV 280

RESULT 4
TN10_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein).
DE TNFSF10 OR TRAIL.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis."
RL Immunity 3:673-682(1995).
CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDESPREAD.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL: U37522; AAC52345.1; -
DR MGD; MGI:107414; TNfsf10.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR00478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.
DR Cytokine; Transmembrane; Signal-anchor; Apoptosis.
KW DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.7%; Score 248; DB 1; Length 291;
Best Local Similarity 25.4%; Pred. No. 7.7e-14;
Matches 79; Conservative 52; Mismatches 100; Indels 80; Gaps 13;

QY 46 RSMFVALLGLG-LGVVVCVALFFYFRAQMD--PNRISEDTGHCIVRIILRLHENADFOT 102
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 17 RMVICIVLQVLQAVSVAVTYVTNELKQMDKYKGLACFSK-----TDEDFWDS 71

QY 103 TLESQDTKLIPDSRRIRK-----QAFO-----GAVQKEL 131
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 72 T-----DGEILNRCLQVKRQLYQLEEVTLRTFDITVPEKQLSTPPLPRGRPKVA 127

QY 132 QHIVGQHIHRAEKAMVDGSLDLAKRSKLEAQFAHLTNATDIPSGSHKVSLSWVHDR 191
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 128 AHITGITR-RSNSALI-----PISKDGKTLGQ-----KTESWESSR 162

QY 192 -GWAKISNMTFSNGKLIVNODGFYLYANICPRRHETSGDLATEYL-----QLMVYV 242
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 163 KGHSLNHLVFLRNGELVIEQGLYIYISQTYFRFQAEQ--ASKWSKDKVTKQLVQYI 220

QY 243 TKTSIKIPSSHTLMKGSTKYNSGSEFFHYSINVGFFKLRGEEISIEVSNPLDPPD 302
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 221 YKVT-SYPDPVLMKSARNCSWRSRDAEYGLYISQGIPELKENDRIFSVSVTNEHLMDLD 279

QY 303 QDATYFGAFKV 313
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 280 QEASFFGAFLI 290

RESULT 5
FASL_HUMAN STANDARD; PRT; 281 AA.
AC P48023;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FAS antigen ligand (Apoptosis antigen ligand) (APTL) (CD178 antigen).
DE TNFSF6 OR APTLGI OR FASL.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes."
RL J. Exp. Med. 181:71-77(1995).
RN [2]
SEQUENCE FROM N.A.
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FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 281 AA; 31485 MW; ABA6EB358246E9BB CRC64;

Query Match 11.2%; Score 189; DB 1; Length 281;
Best Local Similarity 21.7%; Pred. No. 7.6e-09;
Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

QY 22 PGAPHEGPIHAPPPAP-----HOPPAASRS-----MFVALLGLIGGVVCS 63
DB 46 PPPPPPLPPPPPPPLPLPLPLPKKRGHSTGLCLLVNFMFVLVALVGLG----- 100
QY 64 VALFFPRAQMDPNRISEGDTHCIYRILRLHENDFOOTFILESODTKLPDSCRRKQAF 123
DB 101 --MFQLFHQ-----KELAELESTSMHTA----- 124
QY 124 QGAVOKELQHLVGSOHIRAEKAMVDGWSLWLAKSKLEAQAOPFAHLT--INATDIPSGSHK 181
DB 125 -SSLEKQIGH-----PSPPEKKELKRVHLTKSNSRNP----- 159
QY 182 VLSLSSWYHDSRGWAKISNNFTSNGKLIYNQDGFYIYANICFRHHETSGLDLEYQLMAY 241
DB 160 --LEWEDTYGIVLGSVKYKKGGLVINETGLYFYVSKYVPGQSCNN-----LPLSHK 210
QY 242 VTKTSIKIPSHTKMGSGTKY-----WCSNSEPHFYSINVGFFKLSRSGEELSIEVSN 295
DB 211 VYMENSKYPQDLVMEGKMSYCTTGOMWARS-----YLGAVFNLTSAHLVYVNVSE 263
QY 296 PSLDDPDQDATYFGAFKV 313
DB 264 LSLVNFEESOFTFGLYKL 281

RESULT 6
FASL_MOUSE STANDARD; PRT; 279 AA.
ID FASL_MOUSE AC PA1047; Q61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FAS antigen ligand.
GN TNFSF6 OR APTLGI OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=9418517; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RN STRAIN=C57BL/6;
RC TRIMIN-C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Petisch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=9519608; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RN

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CC EMBL; 248469; CAA88363.1; -  
 CC HSP; P29965; IALY.  
 CC InterPro; IPR003263; TNF\_5.  
 CC InterPro; IPR000478; TNF\_family.  
 CC Pfam; PF00229; TNF; 1.  
 CC ProDom; PD008600; TNF\_5; 1.  
 CC SMART; SM00207; TNF; 1.  
 CC PROSITE; PS00251; TNF\_1; 1.  
 CC PROSITE; PS00049; TNF\_2; 1.  
 CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.  
 KW CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1 22  
 FT TRANSMEM 23 46  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 47 261  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 178 218  
 FT CARBOHYD 240 240  
 SQ SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787ED CRC64;

Query Match 10.5%; Score 176.5; DB 1; Length 261;  
 Best Local Similarity 24.2%; Pred. No. 7.9e-08;  
 Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

QY 33 PPPPHAPQPAASRSFVALLGLL-GQVCSVALFFYFRAQMDPNRISEDTGHCYRIL 91  
 DB 8 PPSRVATGPPVSMKIFMYLLVFLVLTOMIGSALFAVYLHRLD--KIEDE-----R 57  
 QY 92 RLHENADFDT--TLESODTKLPDSCRIKQAFQAVQKELQHVGSQHIRAEKAMVDG 149  
 DB 58 NLHEDVFVMTQRCNKGGSLLNCEIRSFEDLVDMQ-----NKEYKKENFE- 112  
 QY 150 SWLDLAKRSKLEAPPAHLTINATIPSGSHKVSLSWYHGRGWAKISN--MTFSNGK-L 206  
 DB 113 -----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYITLSNNLVLENGKQL 161  
 QY 207 IVNQDGFYLYANICRHRHETSGDLATAYLQMLVYVTKYSIKIP--SSHTLMKGGSTKW 264  
 DB 162 AVKROGFYIYQVTPCSNR-----ETLSQAPFIASICLKSPSGSERILLRAANTH-- 212  
 QY 265 SGNSEPHFYSINVGPFKLRSGEISYENSPSLDDPDQDATYFGAFV 313  
 DB 213 SSSKPCQSQSHLGGVFELOSGASVFNVDPSQVSHGCTGFTSFGLLKL 261

RESULT 8  
 ID FASL\_RAT STANDARD; PRT; 278 AA.  
 AC P36940;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FAS antigen ligand.  
 GN TNFSF6 OR APTLIG1 OR FASL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94084792; PubMed=7505205;  
 RA Suda T., Takahashi T., Golstein P., Nagata S.;  
 RT "Molecular cloning and expression of the Fas ligand, a novel member  
 RT of the tumor necrosis factor family.";  
 RL Cell 75:1169-1178(1993).  
 CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
 CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
 CC CYTOTOXIC T CELL-MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
 CC FAS-ANTIGEN-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
 CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
 CC T CELLS, OR BOTH.

CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED  
 CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FROM THE CELL  
 CC SURFACE.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND  
 CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,  
 CC KIDNEY AND LUNG.  
 CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC  
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CC EMBL; U03470; AAC52129.1; -  
 CC HSP; P01375; 4FSV.  
 CC InterPro; IPR003263; TNF\_5.  
 CC InterPro; IPR003636; TNF\_abc.  
 CC InterPro; IPR000478; TNF\_family.  
 CC Pfam; PF00229; TNF; 1.  
 CC ProDom; PD002012; TNF\_abc; 1.  
 CC ProDom; PD008600; TNF\_5; 1.  
 CC SMART; SM00207; TNF; 1.  
 CC PROSITE; PS00251; TNF\_1; 1.  
 CC PROSITE; PS00049; TNF\_2; 1.  
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.  
 FT DOMAIN 1 77  
 FT TRANSMEM 78 99  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT PRO-RICH.  
 FT POLY-PRO.  
 FT BY SIMILARITY.  
 FT DISULFID 199 230  
 FT CARBOHYD 116 116  
 FT CARBOHYD 247 247  
 FT CARBOHYD 257 257  
 FT CARBOHYD 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;  
 SQ SEQUENCE 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;

Query Match 10.4%; Score 175.5; DB 1; Length 278;  
 Best Local Similarity 20.3%; Pred. No. 1e-07;  
 Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

QY 21 GPCAPGEPHAPPPHAPHPAPPAASRSM-----FVALLGLGL 57  
 DB 39 GPGQRPPP-PPPPSPPLPPSPPLPLPLKKNIELMLPVPFFVVALVGMGL 96  
 QY 58 GQVCSVALFFYFRAQMDPNRISEDTGHCYRILRLHENADFDTTLESQDTKLIPDSCR 117  
 DB 97 G-----MYQLFHLQKELAELEFTHSL-RVSSFEKQIANFSTSETKKPRSV----- 143  
 QY 118 RIKQAFQAVQKELQHVGSQHIRAEKAMVDGSLAKRSKLEAPPAHLTINATDIPS 177  
 DB 144 -----AHLTGPR----- 151  
 QY 178 GSHKVSLSWYHGRGWAKISNMTFSNGKLVNODGFYLYANICRHRHETSGDLATAYLQ 237  
 DB 152 -SRSDIT-EMEDTYGTALISGVKKGGLVINEAGLYFVYSKVFYRQSCN-----SQPLS 205  
 QY 238 LMVYVTKTSIKIPSSHTLMKGGSTKYWNSGNSSEPHFYSINVGPFKLRSGEISYENSPS 297  
 DB 206 HKVYM--RNFYPGDLVLMEEKLNCT-TGQIWAHSSVGLAVFNLTADVHLVNIQSLS 262  
 QY 298 LDDPDQDATYFGAFV 313  
 DB 263 LINFESKTFEGLYKL 278

RESULT 9  
 TNFS\_HUMAN STANDARD; PRT; 261 AA.  
 ID TNFS\_HUMAN

AC DT  
 DT 01-APR-1993 (Rel. 25; Created)  
 DT 01-APR-1993 (Rel. 25; Last sequence update)  
 DE 16-OCR-2001 (Rel. 40; Last annotated update)  
 DE CD40 ligand (CD40-L) (TNF-related activation protein) (TRAP) (T cell  
 DE antigen gp39) (CD154 antigen).  
 GN TNFSF5 OR CD40LG OR CD40L OR TRAP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-93049181; PubMed=1280226;  
 RA Graf D., Korthauer U., Mages H.W., Senger G., Krocsek R.A.;  
 RT "Cloning of TRAP, a ligand for CD40 on human T cells";  
 RL Eur. J. Immunol. 22:3191-3194(1992).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-93049181; PubMed=1385114;  
 RA Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,  
 RA Briesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,  
 RA Aruffo A.;  
 RT "The human T cell antigen gp39, a member of the TNF gene family, is a  
 RT ligand for the CD40 receptor: expression of a soluble form of gp39  
 RT with B cell co-stimulatory activity";  
 RL EMBO J. 11:4313-4321(1992).  
 RN [3]  
 RN SEQUENCE FROM N.A., AND VARIANTS HIGH1 128-ARG-GLY-129 AND PRO-235.  
 RX MEDLINE-93145330; PubMed=7678782;  
 RA Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A.,  
 RA Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M.,  
 RA Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;  
 RT "The CD40 ligand, gp39, is defective in activated T cells from  
 RT patients with X-linked hyper-IgM syndrome";  
 RL Cell 72:291-300(1993).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-93094757; PubMed=1281209;  
 RA Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,  
 RA Macduff B.M., Sato T.A., Maliszewski C.K., Fanslow W.C.;  
 RT "Recombinant human CD40 ligand stimulates B cell proliferation and  
 RT immunoglobulin E secretion";  
 RL J. Exp. Med. 176:1543-1550(1992).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-93138085; PubMed=7678552;  
 RA Gauchat J.F.M., Aubry J., Mazzei G.J., Life P., Jomotte T., Elson G.,  
 RA Bonnefoy J.Y.;  
 RT "Human CD40-ligand: molecular cloning, cellular distribution and  
 RT regulation of expression by factors controlling IgE production";  
 RL FEBS Lett. 315:259-266(1993).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RA Shmizu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,  
 RA Matsuda I.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.  
 RX MEDLINE-96131874; PubMed=8589998;  
 RA Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,  
 RA Chess L., Thomas D.;  
 RT "2-A crystal structure of an extracellular fragment of human CD40  
 RT ligand";  
 RL Structure 3:1031-1039(1995).  
 RN [8]  
 RN 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.  
 RX MEDLINE-98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 RT with its receptor CD40";  
 RL Protein Sci. 7:1124-1135(1998).  
 RN [9]  
 RN VARIANTS HIGH1 ARG-36 AND GLY-140.  
 RX MEDLINE-93156839; PubMed=7679206;  
 RA Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,  
 RA Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,  
 RA Krocsek R.A.;  
 RT "Defective expression of T-cell CD40 ligand causes X-linked  
 RT immunodeficiency with hyper-IgM";  
 RL Nature 361:539-541(1993).  
 RN [10]  
 RN VARIANTS HIGH1 GLU-123.  
 RX MEDLINE-93156840; PubMed=8094231;  
 RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,  
 RA de Saint Basile G.;  
 RT "CD40 ligand mutations in X-linked immunodeficiency with hyper-IgM";  
 RL Nature 361:541-543(1993).  
 RN [11]  
 RN VARIANTS HIGH1 PRO-155; ASP-211 AND VAL-227.  
 RX MEDLINE-93174270; PubMed=7679801;  
 RA Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,  
 RA Copeland N.G., Bedell M.A., Edelhoff S., Distche C.M.,  
 RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;  
 RT "CD40 ligand gene defects responsible for X-linked hyper-IgM  
 RT syndrome";  
 RL Science 259:990-993(1993).  
 RN [12]  
 RN VARIANTS HIGH1 ALA-126; ARG-140 AND GLU-144.  
 RX MEDLINE-95233438; PubMed=7717401;  
 RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnoli D.,  
 RA Gilliani S., Mantuano E., Fasth A., Andersson B., Zegers B.J.M.,  
 RA Cavagni G., Reznick I., Levy J., Zan-Bar I., Porat Y., Alro P.,  
 RA Plebani A., Vezzoni P., Notarangelo L.D.;  
 RT "Characterization of nine novel mutations in the CD40 ligand gene in  
 RT patients with X-linked hyper-IgM syndrome of various ancestry";  
 RL Am. J. Hum. Genet. 56:898-906(1995).  
 RN [13]  
 RN VARIANTS HIGH1 PRO-155 AND VAL-227, AND VARIANT ARG-219.  
 RX MEDLINE-96133533; PubMed=8550833;  
 RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,  
 RA Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.;  
 RT "A single strand conformation polymorphism study of CD40 ligand.  
 RT Efficient mutation analysis and carrier detection for X-linked hyper  
 RT IgM syndrome";  
 RL J. Clin. Invest. 97:196-201(1996).  
 RN [14]  
 RN VARIANTS HIGH1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.  
 RX MEDLINE-97295077; PubMed=9150729;  
 RA Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer M.,  
 RA Yata J.-I., Ochi H.D.;  
 RT "Mutations of the CD40 ligand gene in 13 Japanese patients with  
 RT X-linked hyper-IgM syndrome";  
 RL Hum. Genet. 99:624-627(1997).  
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-  
 CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.  
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+  
 CC T-LYMPHOCYTES.  
 CC -1- DISEASE: DEFECTS IN TNFSF5 ARE THE CAUSE OF AN X-LINKED  
 CC IMMUNODEFICIENCY WITH HYPER-IgM (HIGM1); AN IMMUNOGLOBULIN ISOTYPE  
 CC SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM  
 CC IgM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES  
 CC PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)  
 CC RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING  
 CC PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO  
 CC CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH  
 CC INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,  
 CC WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -1- DATABASE: NAME=CD40Lbase;  
 CC NOTE-European CD40L defect database (mutation db);



Db 112 -----MOKGQDPRVAHVISEAS-----SSTASVLQW-APKGYTITSSNLVTLENGKQ 159

Qy 206 LIVNQDGFYIYANICFRHETSGDLATEYLQALVYVTKTSIKIP--SSHFLMKGSGTKY 263

Db 160 LAVKROGLYIYIAVQTFCSNRSEASQAP-----FTASLCLHSPSGSERVLLRAANAR- 211

Qy 264 WSGNSEHFYINVGGFKLRSGEISIEVSNPLSDPDQDQATYFGAFKV 313

Db 212 -SSSKPCQOQSHLGGVFLHPLGASVFVNDPDSOVSHGTGFTSGLLKL 260

RESULT 11

TFNA\_CAVPO STANDARD; PRT; 234 AA.

AC P51435;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).

GN TNF OR TNFA.

OS Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.

NCBI\_TaxID=10141;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=HARTLEY; TISSUE=Lung;

RA Yuan H.T., Kelly F.J., Bingle C.D.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=DUNKIN-HARTLEY;

RX MEDLINE=97462215; PubMed=9316485;

RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;

RT "Airway inflammation induced by recombinant guinea pig tumor necrosis factor-alpha.;"

RL Am. J. Physiol. 273:L574-L530(1997).

CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.

CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).

CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING (BY SIMILARITY).

CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC EMBL; U39839; AAB06492.1; -

DR EMBL; U77036; AAB19210.1; -

DR HSSP; P06804; 2TNF.

DR InterPro; IPR003636; TNF\_family.

DR Pfam; PF00229; TNF; 1.

DR PRINTS; PR01234; TNCRSISFCT.

DR PRODOM; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS0049; TNF\_2; 1.

DR PROSITE; PS0049; TNF\_2; 1.

KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.

FT PROPEP 1 79 BY SIMILARITY.

FT CHAIN 80 234 TUMOR NECROSIS FACTOR.

FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DISULFID 147 178 BY SIMILARITY.

SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 8.7%; Score 146; DB 1; Length 234; A

Best Local Similarity 25.4%; Pred. No. 2.7e-05;

Matches 50; Conservative 30; Mismatches 75; Indels 42; Gaps 8;

Qy 134 IVGSQHIAEAKAMVDCSWLDLAKRSKLEA-----QPPAHLTINATIPSGSHKVSLS 186

Db 55 VIGPQ--REEQFSGPPFRPLAQTULTRSASQNDNDKPVAVVAN-----QQAEEELQ 105

Qy 187 WYHGRGNAKISN-WTFSGNKLIVNODGFYIYANICFRHETSGDLATEYLQALVYVTKT 245

Db 106 WLSKRANALLANGMLSDNQLVVPDGLYIYSQVLFK-----GQCPSYLLLTHTVSRL 160

Qy 246 SIKIPSSHTLN-----KGSSTKYSNGSEEHFYSINVGFFKLSRSGEISIEV 293

Db 161 AVSYPEKVNLLSAIKSPCKQETPEGAERKPW-----YEPIYLGVGFOLQKGRLSAEV 213

Qy 294 SNPSLLD-PQDQATYFG 309

Db 214 NLPQYLDFAFADSGQIYFG 230

RESULT 12

TFN5\_CANFA STANDARD; PRT; 260 AA.

AC O97626;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE CD40 ligand.

GN TNFSF5 OR CD40LG OR CD40L.

OS Canis familiaris (Dog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NCBI\_TaxID=9615;

[1]

RP SEQUENCE FROM N.A.

RA Hosie M.H., Willett B.J.;

RT "Adjuvant properties of canine CD40L.;"

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.

CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).

CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC EMBL; AF086711; AAD04375.1; -

DR HSSP; P29965; ITALY.

DR InterPro; IPR003263; TNF\_5.

DR InterPro; IPR000478; TNF\_family.

DR Pfam; PF00229; TNF; 1.

DR PRODOM; PD008600; TNF\_5; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS0049; TNF\_2; 1.

KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).

Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,  
Ruysschaert M.-R., Fiers W.;  
RT "Molecular cloning of mouse tumour necrosis factor cDNA and its  
RT eukaryotic expression.";  
RT Nucleic Acids Res. 13:4417-4429(1985).  
RN [5]  
SEQUENCE FROM N.A.  
RP MEDLINE=87298639; PubMed=3040015;  
RX MEDLINE=87298639; PubMed=3040015;  
RA Shakhov A.N., Nedospasov S.A.;  
RT "Molecular cloning of genes coding for tumor necrosis factor."  
RT Complete nucleotide sequence of the genome copy of TNF-alpha in  
RT mice.;  
RT Bioorg. Khim. 13:701-705(1987).  
RN [6]  
SEQUENCE FROM N.A.  
RP MEDLINE=88067722; PubMed=3684584;  
RX MEDLINE=88067722; PubMed=3684584;  
RA Samon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;  
RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha  
RT (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";  
RT Nucleic Acids Res. 15:9083-9084(1987).  
RN [7]  
SEQUENCE FROM N.A.  
RP STRAIN=CTS, AND NOD;  
RX MEDLINE=96013654; PubMed=7560085;  
RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,  
RA Takekawa K., Ogihara T.;  
RT "Identification of a new susceptibility locus for insulin-dependent  
RT diabetes mellitus by ancestral haplotype congenic mapping.";  
RN J. Clin. Invest. 96:1936-1942(1995).  
RN [8]  
SEQUENCE FROM N.A.

Sherry B., Juc D.-M., Zentella A., Cerami A.;  
 "Characterization of high molecular weight glycosylated forms of  
 murine tumor necrosis factor.";   
 Biochem. Biophys. Res. Commun. 173:1072-1078(1990).  
 [9]  
 SEQUENCE OF 70-87.  
 MEDLINE-89380231; PubMed-2777790;  
 Cseh K., Beutler B.;  
 "Alternative cleavage of the cachectin/tumor necrosis factor  
 proteolytic results in a larger, inactive form of secreted protein.";   
 J. Biol. Chem. 264:16256-16260(1989).  
 [10]  
 IDENTIFICATION OF MEMBRANE-BOUND FORM.  
 MEDLINE-88165056; PubMed-3349526;  
 Krieglner M., Perez X., Defay K., Albert I., Lu S.D.;  
 "A novel form of TNF/cachectin is a cell surface cytotoxic  
 transmembrane protein: ramifications for the complex physiology of  
 TNF.";   
 Cell 53:45-53(1988).  
 [11]  
 X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.  
 MEDLINE-99190964; PubMed-10089307;  
 Bayens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;  
 "The structure of mouse tumour-necrosis factor at 1.4 A resolution:  
 towards modulation of its selectivity and trimerization.";   
 Acta Crystallogr. D 55:772-778(1999)  
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CONDITIONS.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 PROTEOLYTIC PROCESSING.  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 AND MALNUTRITION.

CC CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC CC

DR EMBL: U06950; AAA18594.1; -

DR EMBL: M13049; AAA040457.1; -

DR EMBL: M11731; AAA040458.1; -

DR EMBL: Y00467; CAA68530.1; -

DR EMBL: X02611; CAA26457.1; -

DR EMBL: M20155; AAA040462.1; ALT\_SEQ.

DR EMBL: M38296; AAA040459.1; -

DR EMBL: D84196; BAA19512.1; -

DR EMBL: D84194; BAA19512.1; JOINED.

DR EMBL: D84195; BAA19512.1; JOINED.

DR EMBL: D84199; BAA19513.1; -

DR EMBL: D84197; BAA19513.1; JOINED.

DR EMBL: D84198; BAA19513.1; JOINED.

DR PIR: A23127; QWMSN.

DR PIR: A22908; A22908.

DR PIR: A25164; A25164.

DR PIR: A27303; A27303.

DR PIR: A34251; A34251.

DR PIR: S03791; S03791.

DR PDB: 2TNE; 12-OCT-99.

DR MGD; MGI:104798; Tnf.

DR InterPro: IPR003636; TNF\_abc.

DR InterPro: IPR000478; TNF\_family.

DR Pfam: PF00229; TNF; 1.

DR PRINTS; PR01234; TNCRSISFCT.

DR ProDom; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF; 1.

DR PROSITE; PS00049; TNF; 2; 1.

DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;

DR PROPEP

CC CC 3D-structure.

CC CC CHAIN 1 79

CC CC TRANSMEM 80 235

CC CC DISULFID 36 56

CC CC CARBOHYD 148 179

CC CC CONFLICT 86 86

CC CC CONFLICT 231 231

CC CC SEQUENCE 235 AA; 25895 MW; 16DD2A9676D68C5D CRC64;

CC CC Query Match 8.4%; Score 141.5; DB 1; Length 235;

CC CC est Local Similarity 25.9%; Pred. No. 6.5e-05;

CC CC Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

QY 163 OPFAHLTINATDIPSGSHKVSLS-SWYHGRGWAKISN-WTFSGKLIYQDGFYLYANI-220

DB 90 KPVARVYAN-----HVEVEQLEWLSQRANALLANGMDLNQVVPADGLYLYVSOV 141

QY 221 CFRHETSGDLATEYLOLMVYVTK-----TSKIPSSHTLMKGGSTKYWSGNS 268

DB 142 LFK-----GQCDDPDLVTHVSRFAISYQEKVNLLSAVSKPCPDTEGAELKFW-----192

QY 269 EFHYISNVGGFFKLRSGEISIEVSNFSLLD-PQDQATYFG 309

DB 193 ---YEPIYGVGVQLEKGDLSAEVNLKPYLDFAESGGVYFG 231

RESULT 14

ID TNFA\_RABIT STANDARD; PRT; 235 AA.

AC P04924;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE GN Tumor necrosis factor precursor (TNF-alpha) (Cachectin).

OS TNF OR TNFA.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-91065534; PubMed-2249779;

RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,

RA Nedospasov S.A.;

RT "Structural analysis of the rabbit TNF locus, containing the genes

RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis

RT factor).";

RL Gene 95:215-221(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-86219712; PubMed-3519138;

RA Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,

RA Wallace R.B.;

RT "Molecular cloning of the gene encoding rabbit tumor necrosis

RT factor.";

RL DNA 5:157-165(1986).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE-86219711; PubMed-3519137;

RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,

RA Hayashi H., Kato M., Seko M.;

RT "Molecular cloning and expression in Escherichia coli of the cDNA

RT coding for rabbit tumor necrosis factor.";

RL DNA 5:149-156(1986).

CC CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE

CC CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF

CC CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF

CC CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION

CC CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE

CC CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN

CC CC CONDITIONS.

CC CC -1- SUBUNIT: HOMOTRIMER.

CC CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN

CC CC EXTRACELLULAR SOLUBLE FORM.

CC CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY

CC CC PROTEOLYTIC PROCESSING.

CC CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING

CC CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH

CC CC AND MALNUTRITION.

CC CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC CC

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CC CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC CC

DR EMBL: M12845; AAA31486.1; -

DR EMBL: M12846; AAA31482.1; -

DR EMBL: M60340; AAA31484.1; -

DR PIR: A25451; A25451.

DR PIR: A25454; A25454.

DR PIR: JS0727; JS0727.

DR HSSP; P06804; 2TNF.

DR InterPro; IPR003636; TNF\_abc.

DR InterPro; IPR000478; TNF\_family.

DR Pfam; PF00229; TNF; 1.

DR PRINTS; PR01234; TNCRSISFCT.

DR ProDom; PD002012; TNF\_abc; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF; 1.

DR PROSITE; PS00049; TNF; 2; 1.

KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.

FT PROPEP 1 79





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 102.166 Seconds  
(without alignments)  
536.769 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEGG.....LLDPDQDATYGAFAKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Archived: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1422	84.4	270	4	Q96Q17
2	1409	83.6	313	11	Q9R1Y0
3	1396.5	82.9	318	11	Q9ESE2
4	1271	75.4	287	11	Q9JJK9
5	909	53.9	199	11	Q9JJK8
6	262	15.5	53	11	Q9JZ19
7	240.5	14.3	214	13	Q9DDZ5
8	216.5	12.8	287	13	Q9OWT9
9	200	11.9	282	6	Q9BEA8
10	200	11.9	282	6	Q9SM04
11	199	11.8	282	6	Q95N10
12	186	11.0	280	6	Q9MYL6
13	184.5	10.9	280	6	Q9BDM5
14	182.5	10.8	280	6	Q9BDN1
15	169.5	10.1	261	6	Q9BDN3
16	167.5	9.9	261	6	Q9BDM3

17	155.5	9.2	261	6	Q9BDC7
18	155	9.2	272	13	Q9I8D8
19	145.5	8.6	239	11	Q9QYH9
20	145	8.6	174	4	Q95150
21	144	8.5	232	11	Q35853
22	143	8.5	240	6	Q9BDM7
23	139.5	8.3	215	11	Q99ND1
24	137.5	8.2	156	11	Q912L4
25	136	8.1	234	6	Q28320
26	134.5	8.0	310	11	Q9JMI0
27	134	8.0	157	4	Q43647
28	134	8.0	204	4	Q96LD2
29	133	7.9	149	6	Q97543
30	133	7.9	191	6	Q9MY22
31	133	7.9	232	4	Q9UIV3
32	131.5	7.8	216	11	Q70332
33	130	7.7	217	11	Q9ERG6
34	128	7.6	234	6	Q9RTJ3
35	127.5	7.6	217	6	Q9BEC5
36	127.5	7.6	235	11	Q9J127
37	127.5	7.6	235	11	Q9J126
38	127.5	7.6	310	11	Q9JMI1
39	126	7.5	149	6	Q97538
40	126	7.5	149	6	Q9RTG8
41	125	7.4	216	6	Q9BEC9
42	124	7.4	250	6	Q9XT47
43	120.5	7.2	217	6	Q9BEG1
44	120.5	7.2	217	6	Q9BEG0
45	120	7.1	260	11	Q9Z2V2

## ALIGNMENTS

### RESULT 1

Q96Q17 PRELIMINARY; PRT; 270 AA.  
AC Q96Q17;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE FRANKL 2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ikeda T., Kuroyama H., Hirokawa K.;  
RT "Human RANKL isoform.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB061227; BAB71768.1; -  
SQ SEQUENCE 270 AA; 30522 MW; 5C7754CE32E6F368 CRC64;

Query Match 84.4%; Score 1422; DB 4; Length 270;  
Best Local Similarity 100.0%; Pred. No. 1.1e-121;  
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	48	MFVALLGIGLGVVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDTTLESQ	107
Db	1	MFVALLGIGLGVVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDTTLESQ	60
QY	108	DTKLIPDSRRIKQAFQGVQKLOHIVGSHIRAEKAMVDGSLDLAKRSKLEAOPFAH	167
Db	61	DTKLIPDSRRIKQAFQGVQKLOHIVGSHIRAEKAMVDGSLDLAKRSKLEAOPFAH	120
QY	168	LTINATIPSGSHKVSLSWYHDSRWAKISNMTFSNGLIVNQDGFYLLYANICFRHET	227
Db	121	LTINATIPSGSHKVSLSWYHDSRWAKISNMTFSNGLIVNQDGFYLLYANICFRHET	180
QY	228	SGDLATYQLMVTYTKTSIKIPSSHTLMKGGSTKYSERHFYSINVGGEFKLSGE	287
Db	181	SGDLATYQLMVTYTKTSIKIPSSHTLMKGGSTKYSERHFYSINVGGEFKLSGE	240

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Q9ESE2 PRELIMINARY; PRT; 318 AA.
AC Q9ESE2;
DT 01-WAR-2001 (TREMBLrel. 16, Created)
DT 01-WAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND.
DE Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL J. Bone Miner. Res. 15:2178-2186(2000).
DR EMBL: AF187319; AACG17031.1; -
DR HSSP; P50591; 1D0G.
DR InterPro: IPR003263; TNE_5.
DR InterPro: IPR000478; TNE_family.
DR Pfam: PF00229; TNE_1.
DR ProDom: PD008600; TNE_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 318 AA; 35370 MW; 4B874AD706AD098F CRC64;

Query Match 82.9%; Score 1396.5; DB 11; Length 318;
Best Local Similarity 82.4%; Pred. No. 3e-119;
Matches 262; Conservative 19; Mismatches 36; Indels 1; Gaps

QY 1 MRRASRDYKYLGRSEMGGPGAPGHEGPLH-APPPAPHPQPPAASRMFVALLGLGLGQ 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRRANDYGYLGRSEMGSCPGVHEGPLHPAPAPAPPAPPAASRFWFLALLGLGLGQ 60

QY 60 VVCSVALFFYFRAQMDPNRISEDTGTHCIYVILRLHENADFQDTTSLSDTKLIPDSCRI 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VVCSIALFLYFRAQMDPNRISEDTSCFVILRLRENTGLQDSTLESDTEALPDSCRM 120

QY 120 KQAFQAGVQELQHVGSQHIRAEKAWDGSWLDLAKRSKLEAQPFPHLTINATDIPSGS 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KQAFQAGVQELQHVGPQRFSGVPAMWEGSWLDVARRKPEAQPFPHLTINAADIPSGS 180

QY 180 HRYSLSSWYHDCRWAKISNMTFSNGKLIYNQDGFYILYANICFRHHETSGDLATEYLQM 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 HRYSLSSWYHDCRWAKISNMTLSNGLRVNQDGFYILYANICFRHHETSGSVADYLQM 240

QY 240 VYVTKTSIKIPSSHTLMKGSTKYWGSNSEFHPYSINVGFFKLRGEEISIEVSNPSSL 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VYVTKTSIKIPSSHNLKMGSTKNWGSNSEFHPYSINVGFFKLRAGEEISVQVSNPSSL 300

QY 300 DPQDQATYFGAFKVRDID 317
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 DPQDQATYFGAFKVRDID 318

RESULT 4
Q9JUK9 PRELIMINARY; PRT; 287 AA.
AC Q9JUK9;
ID Q9JUK9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 2.
DE TNFSF11 OR RANKL 2.
GN TNFSF11 OR RANKL 2.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21150053; PubMed=11250921;

```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bobe J., Goetz F.W.;  
RT "Molecular cloning and expression of a TNF receptor and two TNF  
ligands in the fish ovary."  
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).  
DR EMBL: AF250041; RAG47640.1; -;  
DR HSSP: P50591; ID06.  
DR 2FIN; ZDB-GENE-010801-1; tnfsf101.  
DR InterPro: IPR003263; TNF\_5.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR ProDom: PD002012; TNF\_abc; 1.  
DR ProDom: PD008600; TNF\_5; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
DR SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;  
Query Match 14.3%; Score 240.5; DB 13; Length 214;  
Best Local Similarity 28.6%; Pred. No. 5.4e-14;  
Matches 61; Conservative 50; Mismatches 83; Indels 19; Gaps 5;  
QY 118 RIKAFQAGVOKELQHVQSHIRAEKAMVDGSLDLAK-RSKLEAPPEAHLTINATDIP 176  
Db 2 KLAEGIKAYISKVYDSIISKQTLHAARTQTHSYNTGSKFMTVMQPSAHLTLSSASN 61  
QY 177 S-----GSHKVSLSWYHGRGWAKISNMTFSGKLIYNQDGFYIYLANICF 222  
Db 62 SRPOSDMHQPOFDLHQSRHPVHTWANKSGFAHLYNTLNGRLVRQDGRYIYSQYVF 121  
QY 223 RHETS-GDLATEYLQLMVYV-TKTSIKIPSSHTLMKGGSTKYWSGSEHFYSINVGGF 280  
Db 122 RYPSDSQSSVSHQVOCYIKTSLNPIQ--LLKGVGTKWAPDAEYALHVSVOGGL 179  
QY 281 FKLRSGEISIEVNSPLDPPQDATYFGAFKV 313  
Db 180 FELRAGDEVFVSVPSTMTVYGEDSSVYFGAPRL 212  
RESULT 8  
Q90WT9 PRELIMINARY; PRT; 287 AA.  
AC Q90WT9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
TNF-RELATED APOPTOSIS INDUCING LIGAND.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bridgman J.T., Johnson A.L.;  
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen  
ovary."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY057941; AAL23702.1; -;  
DR SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;  
Query Match 12.8%; Score 216.5; DB 13; Length 287;  
Best Local Similarity 24.7%; Pred. No. 1.3e-11;  
Matches 61; Conservative 57; Mismatches 104; Indels 25; Gaps 6;  
QY 80 SEDGTHCIYRIURLHENADFOTTLIESQDTKLIPDSRRIRKQAFQAGVOKELQHVQSH 139  
Db 51 SSELRLCLINQOQEGSLEEL-----ISNQSLKLANWIKAYVATVTENVISRSV 102

QY 140 I-RAKAWYDGSWLDLAKSKLEAPPEAHLTINATDIP-----SGSHKVSLSW 187  
Db 103 VNEAKSYFNISEGQVA--TKLGKPSAHLIFRPQPAQDSSRRFGNLSOSCEHAITRW 160  
QY 188 YHDRGWAKISNMTFSGKLIYNQDGFYIYLANICFRRHETSGLATEYLQLMVYV-TKTS 246  
Db 161 EDSTHSHLQNTYRDGRLVRNQAGYVYSQIYFRYSRDGAGARVSPQVOCINWRTS 220  
QY 247 IKIPSSHTLMKGGSTKYWSGSEHFYSINVGGFFLKRSGEISIEVNSPLDPPQDAT 306  
Db 221 YSQPI--LLKGVGTRCWAPEAGLYGLHLYQGLFELKAGDELFSVSSLAIDYSDAAS 278  
QY 307 YFGAFKV 313  
Db 279 YFGAPRL 285  
RESULT 9  
Q9BEA8 PRELIMINARY; PRT; 282 AA.  
AC Q9BEA8;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
FAS-LIGAND (FAS LIGAND).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-2132533; PubMed-11429161;  
RA Muneta Y., Shimoji Y., Inumaru S., Mori Y.;  
RT "Molecular cloning, characterization, and expression of porcine Fas  
ligand (CD95 ligand)."  
RL J. Interferon Cytokine Res. 21:305-312(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Tsuyuki S., Kono M., Bloom E.T.;  
RT "Cloning and potential utility of porcine Fas ligand: overexpression  
in porcine cells protects them from attack by human cytolytic cells."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB027297; BAB40919.1; -;  
DR EMBL: AF397407; AAK84408.1; -;  
DR HSSP: P01375; 4TSV.  
DR InterPro: IPR003263; TNF\_5.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF; 1.  
DR PRINTS: PR01234; TNECROSISFCT.  
DR ProDom: PD002012; TNF\_abc; 1.  
DR ProDom: PD008600; TNF\_5; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
SQ SEQUENCE 282 AA; 31756 MW; 6743DAA1145671FB CRC64;  
Query Match 11.9%; Score 200; DB 6; Length 282;  
Best Local Similarity 23.0%; Pred. No. 3.9e-10;  
Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;  
QY 22 PGAPHEGLHAPPPPPHAPHPAPAA-----SRSM-----FVA 51  
Db 37 PGRP--GQRRPPPPPPPPPPPPPTLLPSRPLPLPPPSLKKKDHNGAGLCLLVNFWFWLVA 94  
QY 52 LLGLGLGVGVCSVALFFVYFRAQMDPNRISDGTCHYIRILRLHENADFOTTLIESQDTKL 111  
Db 95 LVGLGLG-----MFQFLHLOKE-----LTLEASASQRT----- 124  
QY 112 IPDSCRRIKQAFQAGVOKELQHVQSHIRAEKAMVDGSLDLAKSKLEAPPEAHLT-- 169  
Db 125 -----ESSLEKQIGHNLPSEKK-----ELRKVAHLTK 153

[illegible]

RESULT	10
Q95M04	
ID	PRELIMINARY; PRT; 282 AA.
Q95M04:	
01-DEC-2001	(T+EMBLrel. 19, Created)
01-DEC-2001	(T+EMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (T+EMBLrel. 19, Last annotation update)
DE	FAS-LIGAND.
GN	PASL.
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBII_Taxid=9823;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BRED LANDRACE X LARGE YORKSHIRE WHITE (LM); TISSUE=LIVER;
RA	*Genetic-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
RT	Motomic Sequence Analysis of Pig Fas-Ligand Gene.;"
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AB069764; BAB64291.1;
DW	EMBL: AB069764; BAB64291.1;
SQ	SEQUENCE 282 AA; 31722 MW; E54774EBF455127B CRC64;
Query Match	11.9%; Score 200; DB 6; Length 282;
Best Local Similarity	23.0%; Pred. No. 3.9e-10;
Matches	76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;

```

RESULT 11
Q95N10
  ID Q95N10      PRELIMINARY;      PRT;      282 AA.
  AC Q95N10;
  DT 01-DEC-2001 (TRENBLrel. 19, Created)
  DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
  DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
  DE FAS LIGAND.

```

[illegible]

```

RESULT 12
ID Q9MYL6
AC Q9MYL6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FAS LIGAND.
GN PT-FASL OR CM-FASL OR RM-FASL.
OS Macaca nemestrina (Pig-tailed macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus mo
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecia
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9545, 9541, 9544;
ID [1]
RN SEQUENCE FROM N.A.
RC SPECIES=M. nemestrina; STRAIN=PIG-TAILED MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Pig-tailed monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
ID [2]
RN SEQUENCE FROM N.A.
RC SPECIES=M. fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Cynomolgus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
ID [3]
RN SEQUENCE FROM N.A.
RC SPECIES=M. mulatta; STRAIN=RHESUS MONKEY;
RA
RC

```

RP SEQUENCE FROM N.A.  
RC SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;

RP SEQUENCE FROM N.A.  
RC SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;

RA Kirii Y., Inoue T., Yoshino K.;  
RT \*Rhesus monkey Fas ligand mRNA, complete cds.\*;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB035140; BAA30296.1; -  
DR EMBL; AB035138; BAA30294.1; -  
DR EMBL; AB035139; BAA30295.1; -  
DR HSP; P01375; 4TSV.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_abc; 1.  
DR ProDom; PD008600; TNF\_5; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS0049; TNF\_2; 1.  
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 11.0%; Score 186; DB 6; Length 280;  
Best Local Similarity 22.1%; Pred. No. 7.4e-09;  
Matches 69; Conservative 44; Mismatches 103; Indels 96; Gaps 11;

QY 22 PGAPHEGLHAPPPAP--HPPAASRS-----HPPAASRS-----MFVALLGLGLGOVCS 63  
DB 45 PPPPPPPPLPPPPSPPLPLPLPLKRGHSTGLCLLVFMFVVALVGLGLG-----99  
QY 64 VALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADPQDTTLESQDTKLIPDSRRIKQAF 123  
DB 100 --MFOLFHLQ-----KELALRESTSQKHTA-----123  
QY 124 QGAVQKELQHVIGSQHRAEKAMVDGSLDLAKRSKLEAQPFAHLT--INATDIPSGSHK 181  
DB 124 --SLEKQIGH-----PSPPEKKEQKVAHLTKGPNRSRMP-----158  
QY 182 VLSLWYHGRGKAKISNMTFSGKLVNODGFYLYANICFRHETSGDLATEYLQLMVY 241  
DB 159 ---LEWEDYIGVLLSGVKYKGLVINETGLYFVYSKYFR-----GQSCIN-LPLSHK 209  
QY 242 VTKTSIKPSSHTLMKGGSTKYWSGNSEPHFYSINVGPFKLRSGEIEISIEVNSPILDP 301  
DB 210 VYMRNSKYPQDLVMEGKMNSYCT-TGOMWAHSSYLGAVENTLSADHLVYVNSLSLVNF 268  
QY 302 DQDATYEGAFKV 313  
DB 269 EESQTFFGLYKL 280

RESULT 13  
Q9BDM5

Q9BDM5 PRELIMINARY; PRT; 280 AA.  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE FAS ANTIGEN CD95.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21383618; PubMed-11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate  
RT Fas/Fas-ligand and co-stimulatory molecules.";  
RL Immunogenetics 53:315-328(2001).  
DR EMBL; AF344856; AAK37539.1; -  
DR HSP; P01375; 4TSV.  
DR InterPro; IPR002965; P-rich\_extensn.  
DR InterPro; IPR003263; TNF\_5.

DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01217; PRICEXTENS.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_abc; 1.  
DR ProDom; PD008600; TNF\_5; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS0049; TNF\_2; 1.  
SQ SEQUENCE 280 AA; 31377 MW; 729EA61436F2D398 CRC64;

Query Match 10.9%; Score 184.5; DB 6; Length 280;  
Best Local Similarity 22.4%; Pred. No. 1e-08;  
Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

QY 22 PGAPHEGLHAPPPAPPHOPP-----AASRS-----MFVALLGLGLGOVVC 62  
DB 46 PPPPPPPPLPPPPPPPLPLPLPLKRGHSTGLCLLVFMFVVALVGLGLG-----99  
QY 63 SVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADPQDTTLESQDTKLIPDSRRIKOA 122  
DB 100 --MFOLFHLQ-----KELALRESTSQKHTA-----123  
QY 123 FQAVQKELQHVIGSQHRAEKAMVDGSLDLAKRSKLEAQPFAHLT--INATDIPSGSH 180  
DB 124 --SLEKQIGH-----PSPPEKKEQKVAHLTKGPNRSRMP-----158  
QY 181 KVSLSWYHGRGKAKISNMTFSGKLVNODGFYLYANICFRHETSGDLATEYLQLMVY 240  
DB 159 ---LEWEDYIGVLLSGVKYKGLVINETGLYFVYSKYFR-----GQSCIN-LPLSH 208  
QY 241 VYTKTSIKPSSHTLMKGGSTKYWSGNSEPHFYSINVGPFKLRSGEIEISIEVNSPILDP 300  
DB 209 VYMRNSKYPQDLVMEGKMNSYCT-TGOMWAHSSYLGAVENTLSADHLVYVNSLSLVN 267  
QY 301 PDQDATYEGAFKV 313  
DB 268 EESQTFFGLYKL 280

RESULT 14  
Q9BDN1

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AC Q9BDN1  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE CD95L PROTEIN.  
GN CD95L.  
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9531;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21383618; PubMed-11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate  
RT Fas/Fas-ligand and co-stimulatory molecules.";  
RL Immunogenetics 53:315-328(2001).  
DR EMBL; AF344847; AAK37606.1; -  
DR HSP; P01375; 4TSV.  
DR InterPro; IPR002965; P-rich\_extensn.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01217; PRICEXTENS.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_abc; 1.

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DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067BD7D398 CRC64;

Query Match      10.8%; Score 182.5; DB 6; Length 280;
Best Local Similarity 22.4%; Pred. No. 1.5e-08;
Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

QY 22 PGAPHEGLHAPPPAPAPHOPP-----AASRS-----MFVALLGLGLGVVC 62
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 46 PPPPPPPPL-PPPPPPPLPLPLPLKRGHSTGLCLLVFMFVVALVGLGLG----- 99
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 SVALLFFPRAQMDPNRISDGHCHYRILRLHENADFDFTLESQDTKLIPDSCKRIKA 122
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123 FOGAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHILT--INATDIPSGSH 180
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Db 124 --SSLEKQIGH-----PSPPEKKEQKVAHILTKPNSRSM----- 158

QY 181 KVSLSWSYHRCWAKISNMTFNGKLIIVNODGFYIYANICFRHHTSGDLATEYLQLMV 240
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Db 159 ----LEWEDTYGIVLLSGVKYKGGIVNETGLYFYVKYFR-----GQSCTN-LPLSH 208

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Db 209 KYIMRNKYPQDLVMMHGKMSYCT-TGQMAHSSYLGAVFNLSTDRHLYVNVVSELV 267

QY 301 PQDATYFGAFKV 313
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Db 268 FEESQTFGLYKL 280

RESULT 15
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AC Q9BDN3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CD154 PROTEIN.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
NCBI_TaxID=9483;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344844; RAK37603.1;
DR HSP; P29965; IALX.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 261 AA; 29360 MW; 10CA588D923754EB CRC64;

Query Match      10.1%; Score 169.5; DB 6; Length 261;
Best Local Similarity 24.6%; Pred. No. 2.1e-07;
Matches 71; Conservative 55; Mismatches 120; Indels 43; Gaps 15;

QY 33 PPPPAPHPAPASRSMFVALLGLL-GVVCSVALFFYFRAQMDPNRISDGHCHYRIL 91
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Db 8 PVPRSAATGPPVSMKIFMYLLTVFLITQMGSAFVYLHRRLD--KIEDE-----R 57

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QY 150 SWLDLAKRSKLEAQPFAHILTINATDIPSGSHKVSLSWSYHRCWAKISN--WTFSGK-L 206
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Db 110 SF-EMQKQDQ-NPQIAAHVISEAS-----SKTTSVLQW-AERGYPTMSNNLVLEKQL 161
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QY 207 IVNODGFYIYANICFRHHTSGDLATEYLQLMVYVYTKTSIKIPS--SHTLMKGGSTKYW 264
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Db 162 TVARQGLTIYIAQVTFCSNREASSQAP-----FIASCLKRPNPFERILLRAANTH-- 212
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 265 SGNSEFHYFSINVGFFKLRSGEEISIEVSNPSLLDPPDQDATYFGAFKV 313
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Search completed: October 10, 2002, 16:03:00  
Job time : 107.166 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 38.1928 Seconds  
(without alignments)  
202.732 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTYLRCSEEMGG.....LLDPDQDATYGAFFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Aligned: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
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5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1685	100.0	317	3	US-08-996-139-13
2	1685	100.0	317	4	US-08-995-659-13
3	1685	100.0	317	4	US-09-215-649A-13
4	1685	100.0	317	4	US-09-052-521C-4
5	1417.5	84.1	316	2	US-08-842-842-7
6	1417.5	84.1	316	4	US-08-989-362-2
7	1417.5	84.1	316	4	US-09-052-521C-2
8	1326.5	78.7	294	3	US-08-996-139-11
9	1326.5	78.7	294	4	US-08-995-659-11
10	1326.5	78.7	294	4	US-09-215-649A-11
11	251.5	14.9	279	4	US-09-072-993C-3
12	251.5	14.9	281	1	US-08-670-354-2
13	251.5	14.9	281	3	US-08-584-031-1
14	251.5	14.9	281	3	US-08-780-496-1
15	251.5	14.9	281	4	US-08-883-086-10
16	251.5	14.9	281	4	US-09-320-424-2
17	251.5	14.9	281	4	US-09-333-593A-6
18	251.5	14.9	281	5	PCT-US96-10895-2
19	248	14.7	291	1	US-08-670-354-6
20	248	14.7	291	4	US-09-320-424-6
21	248	14.7	291	5	PCT-US96-10895-6
22	236.5	14.0	253	4	US-09-320-424-11
23	236.5	14.0	256	4	US-09-320-424-13
24	231.5	13.7	177	4	US-09-105-343A-7
25	226.5	13.4	183	4	US-09-105-343A-8
26	189	11.2	281	2	US-08-810-453-2
27	189	11.2	281	3	US-08-815-190A-2

28	189	11.2	281	4	US-09-290-640-25
29	189	11.2	281	4	US-09-479-524-3
30	189	11.2	281	4	US-08-339-214-8
31	189	11.2	281	4	US-08-339-214-30
32	189	11.2	281	5	PCT-US95-00362-2
33	184.5	10.9	279	4	US-08-339-214-24
34	184.5	10.9	279	4	US-08-339-214-32
35	184.5	10.9	279	5	PCT-US95-00362-5
36	175.5	10.4	278	4	US-08-339-214-16
37	175.5	10.4	278	4	US-08-339-214-26
38	164.5	9.8	376	3	US-08-751-512-8
39	158.5	9.4	261	1	US-07-940-605A-2
40	158.5	9.4	261	1	US-08-184-422-8
41	158.5	9.4	261	1	US-08-360-933A-2
42	158.5	9.4	261	1	US-08-446-923-4
43	158.5	9.4	261	2	US-08-431-055-4
44	158.5	9.4	261	2	US-08-690-096-2
45	158.5	9.4	261	2	US-08-249-189-12

## ALIGNMENTS

RESULT 1  
US-08-996-139-13  
; Sequence 13, Application US/08996139  
; Patent No. 6017729  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent  
; APPLICANT: Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,139  
; FILING DATE: 22 DECEMBER 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/064,671  
; FILING DATE: 14 OCTOBER 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2851-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 317 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-996-139-13

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TELEFAX: (206)233-0644
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-13

Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 9.8e-164;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VCSVALFFYPRAQMDPNRISDGHCHYIRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
QY 121 QAFQAVQKELQIHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFPAHITINATDIPSGSH 180
Db 121 QAFQAVQKELQIHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFPAHITINATDIPSGSH 180
QY 181 KVSLSWYHDRGWAKISNMTFSNGKLIYNQDGFYLLYANICFRHHETSGDLATEYLQLMV 240
Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIYNQDGFYLLYANICFRHHETSGDLATEYLQLMV 240
QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEHFYSINVGFFKLRSGEISIEVSNPSLLD 300
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEHFYSINVGFFKLRSGEISIEVSNPSLLD 300
QY 301 PQDATYFGAFKVRDID 317
Db 301 PQDATYFGAFKVRDID 317

RESULT 3
US-09-215-649A-13
; Sequence 13, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne

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REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2851-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 317 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-215-649A-13

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 9.8e-164;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 VCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFQDTTLESQDTKLIPDSRRK 120

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121 QAFQAVOKELQHVSHIRAEKAWDGSWLDLAKRSKLEAOPFAHLTINATDIPSGSH 180

181 KVSLSWYHDSRWAKISNMTFNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQMV 240  
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241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYINVGFFKLRSGEISIEVSNPSLLD 300  
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301 PQDATYFGAFKVRDID 317  
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301 PQDATYFGAFKVRDID 317

RESULT 4  
US-09-052-521C-4  
Sequence 4, Application US/09052521C  
Patent No. 6316408

GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors  
FILE REFERENCE: A-451Brv  
CURRENT APPLICATION NUMBER: US/09/052,521C  
PRIOR FILING DATE: 1998-03-30  
PRIOR FILING DATE: 1997-06-23  
PRIOR FILING DATE: 1997-04-16  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 317  
TYPE: PRT  
ORGANISM: Human  
US-09-052-521C-4

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 9.8e-164;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRRASRDYTKYLGRSEMGPGAPHEGLHAPPPAPHPAPPAASRSMFVALLGLGQV 60  
|||||  
1 MRRASRDYTKYLGRSEMGPGAPHEGLHAPPPAPHPAPPAASRSMFVALLGLGQV 60

QY 61 VCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFQDTTLESQDTKLIPDSRRK 120  
|||||  
Db 61 VCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFQDTTLESQDTKLIPDSRRK 120

QY 121 QAFQAVOKELQHVSHIRAEKAWDGSWLDLAKRSKLEAOPFAHLTINATDIPSGSH 180  
|||||  
Db 121 QAFQAVOKELQHVSHIRAEKAWDGSWLDLAKRSKLEAOPFAHLTINATDIPSGSH 180

QY 181 KVSLSWYHDSRWAKISNMTFNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQMV 240  
|||||  
Db 181 KVSLSWYHDSRWAKISNMTFNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQMV 240

QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYINVGFFKLRSGEISIEVSNPSLLD 300  
|||||  
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYINVGFFKLRSGEISIEVSNPSLLD 300

QY 301 PQDATYFGAFKVRDID 317  
|||||  
Db 301 PQDATYFGAFKVRDID 317

RESULT 5  
US-08-842-842-7  
Sequence 7, Application US/08842842  
Patent No. 5843678

GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DeWitt Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/842,842  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-451  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 316 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-842-842-7

Query Match 84.1%; Score 1417.5; DB 2; Length 316;  
Best Local Similarity 84.3%; Pred. No. 1.9e-136;  
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLGRSEMGPGAPHEGLHAPPPAPHPAPPAASRSMFVALLGLGQV 59  
|||||  
Db 1 MRRASRDYTKYLGRSEMGPGAPHEGLHAPPPAPHPAPPAASRSMFVALLGLGQV 60

QY 60 VCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFQDTTLESQDTKLIPDSRRK 119  
|||||  
Db 61 VCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFQDTTLESQDTKLIPDSRRK 118

QY 120 QAFQAVOKELQHVSHIRAEKAWDGSWLDLAKRSKLEAOPFAHLTINATDIPSGSH 179  
|||||  
Db 119 QAFQAVOKELQHVSHIRAEKAWDGSWLDLAKRSKLEAOPFAHLTINATDIPSGSH 178

QY 180 HKVSLSSWYHDSRWAKISNMTFNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQMV 239  
|||||

Db 179 HKVTLSWYHNRGAKISNMTLSNGLRVNODGFYLYANICFRHHETSGSVPTDYQLM 238  
Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWNSGFHYSINVGFFKLRSGEISIEVSNPSLL 299  
Db 239 VYVTKTSIKIPSSHTLMKGGSTKYWNSGFHYSINVGFFKLRSGEISIEVSNPSLL 298  
Qy 300 DPQDQATYFGAFKVRDID 317  
Db 299 DPQDQATYFGAFKVRDID 316

## RESULT 6

US-08-989-362-2  
; Sequence 2, Application US/08989362  
; Patent No. 6242586

## GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Mattson, Jeanine D.  
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related  
; TITLE OF INVENTION: Reagents  
; NUMBER OF SEQUENCES: 2

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,362  
; FILING DATE: 12-DEC-1997  
; CLASSIFICATION: 56

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/032,846  
; FILING DATE: 13-DEC-1996

## ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0686

## TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650)852-9196

; TELEFAX: (650)496-1204

## INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 316 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-989-362-2

Query Match 84.1%; Score 1417.5; DB 4; Length 316;  
Best Local Similarity 84.3%; Pred. No. 1.9e-136;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 59  
Db 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 60  
Qy 60 VVCSVALFFYFRAQMDPNRISEDTGHCYRILRLHENAADFQDTLESODTKLIPDSCRRI 119  
Db 61 VVCSIALFLYFRAQMDPNRISEDTGHCYRILRLHENAAGLQDSTLESDT--LPDSCRRI 118  
Qy 120 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLLTNATDIPSGS 179  
Db 119 KOAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQKGPFAQPFALHTINAASIPSGS 178  
Qy 180 HKVLSWYHNRGAKISNMTLSNGLRVNODGFYLYANICFRHHETSGDLATEYLQLM 239

Db 179 HKVTLSWYHNRGAKISNMTLSNGLRVNODGFYLYANICFRHHETSGSVPTDYQLM 238  
Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWNSGFHYSINVGFFKLRSGEISIEVSNPSLL 299  
Db 239 VYVTKTSIKIPSSHTLMKGGSTKYWNSGFHYSINVGFFKLRSGEISIEVSNPSLL 298  
Qy 300 DPQDQATYFGAFKVRDID 317  
Db 299 DPQDQATYFGAFKVRDID 316

## RESULT 7

US-09-052-521C-2  
; Sequence 2, Application US/09052521C  
; Patent No. 6316408

## GENERAL INFORMATION:

; APPLICANT: Boyle, William J.  
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors  
; FILE REFERENCE: A-451Brv  
; CURRENT APPLICATION NUMBER: US/09/052,521C  
; CURRENT FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: 08/880,855

; PRIOR FILING DATE: 1997-06-23

; PRIOR APPLICATION NUMBER: 08/842,842

; PRIOR FILING DATE: 1997-04-16

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 2

; LENGTH: 316

; TYPE: PRT

; ORGANISM: Mouse

US-09-052-521C-2

## Query Match

84.1%; Score 1417.5; DB 4; Length 316;

Best Local Similarity 84.3%; Pred. No. 1.9e-136;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 59  
Db 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 60  
Qy 60 VVCSVALFFYFRAQMDPNRISEDTGHCYRILRLHENAADFQDTLESODTKLIPDSCRRI 119  
Db 61 VVCSIALFLYFRAQMDPNRISEDTGHCYRILRLHENAAGLQDSTLESDT--LPDSCRRI 118  
Qy 120 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLLTNATDIPSGS 179  
Db 119 KOAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQKGPFAQPFALHTINAASIPSGS 178  
Qy 180 HKVLSWYHNRGAKISNMTLSNGLRVNODGFYLYANICFRHHETSGDLATEYLQLM 239  
Db 179 HKVTLSWYHNRGAKISNMTLSNGLRVNODGFYLYANICFRHHETSGSVPTDYQLM 238  
Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWNSGFHYSINVGFFKLRSGEISIEVSNPSLL 299  
Db 239 VYVTKTSIKIPSSHTLMKGGSTKYWNSGFHYSINVGFFKLRSGEISIEVSNPSLL 298  
Qy 300 DPQDQATYFGAFKVRDID 317  
Db 299 DPQDQATYFGAFKVRDID 316

## RESULT 8

US-08-996-139-11

; Sequence 11, Application US/08996139

; Patent No. 6017729

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

[illegible]



CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/496,632  
FILING DATE: 29-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/548,368  
FILING DATE: 01-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2835-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-670-354-2

Query Match 14.9%; Score 251.5; DB 1; Length 281;  
Best Local Similarity 24.1%; Pred. No. 1.4e-17;  
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY 42 PAASRSMFVALLGLGQVVCVVALFFYFRAQMD--PNRISEDTGTCIYRILRLHENADF 99  
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACF-----LKED--- 61  
QY 100 QDTTLESQDTKLIPDSCRRIKQAFQAVQKELQHVQSHIRAEKAMVDGSWLDLAKRSK 159  
DB 62 -DSYWDPNDEESMNSPCQVKW-----QLRQLVRKMLRTSEETI-----STVQEKQ 107  
QY 160 LEAQPF-----AHLT-----INATDIPSGSHKVS-----SSWYHDR-GWAKISNM 199  
DB 108 QNISPLVRERGPORVAAHITGTRSRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNL 167  
QY 200 TFSNGKLVNODGFYLYANICFRHHETSGDLATEYLQLMVYVTKSIKIPSSHTLMKGG 259  
DB 168 HLRNGELVIEHKEFYIYSQTYFRQEEIKENTKNDQMVOYIYKYT-SYDPDILLMKSA 226  
QY 260 STKYNSGNSEFFHYISINVGGFFKLRSGEISIEVNSPLDPODDATYFGAFKV 313  
DB 227 RNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

RESULT 13  
US-08-584-031-1  
Sequence 1, Application US/08584031A  
Patent No. 6030945  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: APO-2 LIGAND  
FILE REFERENCE: 11669.22US03  
CURRENT APPLICATION NUMBER: US/08/584,031A  
CURRENT FILING DATE: 1996-01-09  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-584-031-1

Query Match 14.9%; Score 251.5; DB 3; Length 281;  
Best Local Similarity 24.1%; Pred. No. 1.4e-17;  
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY 42 PAASRSMFVALLGLGQVVCVVALFFYFRAQMD--PNRISEDTGTCIYRILRLHENADF 99

DB 10 PSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACF-----LKED--- 61  
QY 100 QDTTLESQDTKLIPDSCRRIKQAFQAVQKELQHVQSHIRAEKAMVDGSWLDLAKRSK 159  
DB 62 -DSYWDPNDEESMNSPCQVKW-----QLRQLVRKMLRTSEETI-----STVQEKQ 107  
QY 160 LEAQPF-----AHLT-----INATDIPSGSHKVS-----SSWYHDR-GWAKISNM 199  
DB 108 QNISPLVRERGPORVAAHITGTRSRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNL 167  
QY 200 TFSNGKLVNODGFYLYANICFRHHETSGDLATEYLQLMVYVTKSIKIPSSHTLMKGG 259  
DB 168 HLRNGELVIEHKEFYIYSQTYFRQEEIKENTKNDQMVOYIYKYT-SYDPDILLMKSA 226  
QY 260 STKYNSGNSEFFHYISINVGGFFKLRSGEISIEVNSPLDPODDATYFGAFKV 313  
DB 227 RNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

RESULT 14  
US-08-780-496-1  
Sequence 1, Application US/08780496  
Patent No. 6046048  
GENERAL INFORMATION:  
APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim  
TITLE OF INVENTION: APO-2 Ligand  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,496  
FILING DATE: 08-Jan-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P0978P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5416  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-780-496-1

Query Match 14.9%; Score 251.5; DB 3; Length 281;  
Best Local Similarity 24.1%; Pred. No. 1.4e-17;  
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY 42 PAASRSMFVALLGLGQVVCVVALFFYFRAQMD--PNRISEDTGTCIYRILRLHENADF 99  
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACF-----LKED--- 61  
QY 100 QDTTLESQDTKLIPDSCRRIKQAFQAVQKELQHVQSHIRAEKAMVDGSWLDLAKRSK 159  
DB 62 -DSYWDPNDEESMNSPCQVKW-----QLRQLVRKMLRTSEETI-----STVQEKQ 107  
QY 160 LEAQPF-----AHLT-----INATDIPSGSHKVS-----SSWYHDR-GWAKISNM 199

Db 108 QNISPLVREGRQVAAHITCTGRKSNLTSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167  
Qy 200 TFSNGKLIIVNDGGYYLYANCFRHHETSGDLATEYQLWVYVTKTSIKIPSSHTLMKGG 259  
Db 168 HLRNGELVIHERGFFYYIYSQYFRFQEEIKENTKNDKQMVQYIYKYT-SYDPDILLMKSA 226  
Qy 260 STKYWSGNSEPHFYISINVGGFKLRSGEISIEVSNPSLLDPDQDATYFGAFKV 313  
Db 227 RNSCWSKDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

## RESULT 15

US-08-883-086-10  
; Sequence 10, Application US/08883086

; Patent No. 6171787

; GENERAL INFORMATION:

; APPLICANT: WILEY, STEVEN

; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL

; FOR TREATMENT AND DIAGNOSIS OF DISEASE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Addott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/883,086

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Foremski, Priscilla E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 6134.US.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847-937-0378

; TELEFAX: 847-938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 281 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6171787e

US-08-883-086-10

Query Match

Best Local Similarity 14.9%; Score 251.5; DB 4; Length 281;

Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

Qy 42 PAASRSMFVALLGLGVGVCSVALFFFYFQAQMD--PNRISDGTGHCYIRILRHENADF 99  
Db 10 PSLGQTCVLIVFTVLLQSLCVANVYVYTNELKQMDKYSKGTACF-----LKED--- 61  
Qy 100 QDTLLESQTKLIPDSCKRIKQAFQAVQKQLQHVGSQHIRAEKAWVDGSLDLAKRSK 159  
Db 62 -DSYWDPNDEESMNSPCQVKW-----QLRLVRKMLRTSEETI-----STVQEKQ 107  
Qy 160 LEAQPF-----AHLT-----INATDIPSGSHKVS-----SSWYHDR-GWAKISNM 199  
Db 108 QNISPLVREGRQVAAHITCTGRKSNLTSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167  
Qy 200 TFSNGKLIIVNDGGYYLYANCFRHHETSGDLATEYQLWVYVTKTSIKIPSSHTLMKGG 259

Db 168 HLRNGELVIHERGFFYYIYSQYFRFQEEIKENTKNDKQMVQYIYKYT-SYDPDILLMKSA 226  
Qy 260 STKYWSGNSEPHFYISINVGGFKLRSGEISIEVSNPSLLDPDQDATYFGAFKV 313  
Db 227 RNSCWSKDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

Search completed: October 10, 2002, 16:03:55

Job time : 42.1928 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 4.02108 Seconds  
(without alignments)  
414.343 Million cell updates/sec

Title: us-09-787-126-34

Perfect score: 74

Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	AA06310	Tetanus toxin epit
2	74	100.0	15	AAW35506	Universal T-cell e
3	74	100.0	15	AAW11505	Tetanus toxoid uni
4	74	100.0	15	AAW67033	Tetanus toxin frag
5	74	100.0	15	AAW71321	Universal helper T
6	74	100.0	15	AAW04051	T-Helper epitope f
7	74	100.0	15	AAW67578	T-cell epitope pep
8	74	100.0	15	AAW73220	Tetanus toxoid epi
9	74	100.0	15	AAW45511	Tetanus P2 epitope
10	74	100.0	15	AAW82637	Tetanus toxoid T c
11	74	100.0	15	AAW92625	Foreign epitope P2

12	74	100.0	15	21	AAW84427	Amino acid sequenc
13	74	100.0	15	21	AAW70300	Clostridium tetani
14	74	100.0	15	21	AAW44763	Tetanus toxoid pro
15	74	100.0	15	22	AAE11763	Clostridium tetani
16	74	100.0	15	22	AAW99515	Vaccine related MH
17	74	100.0	15	22	AAW85701	Amino acid sequenc
18	74	100.0	15	22	AAW8451	Wild-type TT830 (t
19	74	100.0	15	22	AAW61956	Tetanus toxoid uni
20	74	100.0	15	22	AAW20143	Tetanus toxin T-ce
21	74	100.0	15	22	AAW68636	HER-2 B cell pepti
22	74	100.0	15	22	AAW46172	Tetanus toxoid TT8
23	74	100.0	15	22	AAW49071	Tetanus toxoid TT
24	74	100.0	16	18	AAW33445	T-cell stimulatory
25	74	100.0	16	20	AAW29705	Clostridium tetani
26	74	100.0	17	15	AAW62692	Helper T cell epit
27	74	100.0	17	16	AAW82573	Tetanus toxin help
28	74	100.0	17	17	AAW05599	Tetanus toxin help
29	74	100.0	17	17	AAW88395	T-cell antigen TT2
30	74	100.0	17	21	AAW99274	HLA class II bindi
31	74	100.0	17	21	AAW80056	Pathogen derived T
32	74	100.0	17	21	AAW54539	T helper cell (Th)
33	74	100.0	17	21	AAW58768	Unidentified pepti
34	74	100.0	17	22	AAW95516	Vaccine related MH
35	74	100.0	17	22	AAW62904	Amino acid residue
36	74	100.0	17	22	AAW84435	Amino acid sequenc
37	74	100.0	17	22	AAW30941	Amino acid sequenc
38	74	100.0	17	22	AAW31029	Antigenic fragment
39	74	100.0	17	22	AAW31118	Antigenic fragment
40	74	100.0	17	22	AAW15589	Peptide 5 for pept
41	74	100.0	18	20	AAW26607	HIV-derived lipope
42	74	100.0	19	21	AAW99055	HLA class II bindi
43	74	100.0	19	22	AAW99517	Vaccine related MH
44	74	100.0	22	22	AAW46175	Tetanus toxoid 830
45	74	100.0	22	22	AAW46178	Tetanus toxoid 830

## ALIGNMENTS

RESULT 1  
AAW06310  
ID AAR06310 standard; protein; 15 AA.  
XX  
AC AAR06310;  
XX  
DT 04-DEC-1990 (first entry)  
XX  
DE Tetanus toxin epitope.  
XX  
KW Tetanus toxin; vaccine; major histocompatibility complex; MHC;  
KW antimalarial.  
XX  
OS Synthetic.  
XX  
PN EP378881-A.  
XX  
PD 25-JUL-1990.  
XX  
PF 27-DEC-1989; 89EP-0203318.  
XX  
PR 16-NOV-1989; 89IT-0022409.  
PR 17-JAN-1989; 89IT-0019110.  
XX  
(ENIE ) ENIRICERHE SPA.  
XX  
PI Pessi A, Bianchi E, Verdini AS, Corradin G;  
XX  
DR WPI; 1990-225582/30.  
XX  
PT Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used  
PT as universal carriers for prepn. of immunogenic conjugate(s) for  
PT use as vaccines.  
XX

PS Claim 1; Page 17; 20pp; English.

CC Epitopic peptides may be used with synthetic haptens derived from  
 CC a pathogen to generate an immune response to the pathogen.  
 CC Peptides are recognised by numerous T-helper cell clones within  
 CC the context of a wide range of alleles of the human MHC.  
 CC The peptides may be used in an antimalarial vaccine inducing Ab.  
 CC response to P.falciparum.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 3.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
 DB 1 QYIKANSKFIGITEL 15  
 |||||

RESULT 2  
 AAW35506 standard; peptide; 15 AA.

AC AAW35506;

XX 22-APR-1998 (first entry)

DE Universal T-cell epitope peptide SEQ ID NO:8.

XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;  
 KW scaffold; inhibition; metastasis; wound healing; solid phase.  
 KW Unidentified.

OS WO9738011-A1.

XX 16-OCT-1997.

XX 03-APR-1997; 97WO-DE00146.

XX 03-APR-1996; 96DK-0000398.

PA (PEPR-) PEPRSEARCH AS.

PI Heegaard PMH, Jakobsen PH;

XX WPI; 1997-512645/47.

XX Non-dendritic peptide carrier linked to a solid phase - useful as a  
 diagnostic agent and as a scaffold for production of chemical  
 derivatives

XX Example 20; Page 124; 262pp; English.

PS A non-dendritic peptide carrier (A) has been developed which is coupled  
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.  
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary  
 CC structure in a benign buffer after liberation from the solid phase, and  
 CC further the (A)-solid phase complex comprises an immunogenic substance  
 CC and/or an immune mediator coupled on (A). The present sequence  
 CC represents a peptide used in an example from the present invention. An  
 CC (A)-solid phase complex can be used as a scaffold for the production of  
 CC chemical derivatives, characterised by covalently attaching molecules at  
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for  
 CC the incorporation into an Immunostimulating Complex (Iscom) resulting an  
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic  
 CC substances in an aqueous solution by conjugation. (A) derivatised with  
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like  
 CC binding activities can be used for the promotion of cell-attachment to  
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,  
 CC and for promotion of wound healing. Also a derivatised (A) can be used  
 CC for the selection of specifically-binding aptamers or as a diagnostic

CC agent. Such diagnostic-(A) molecules could be used to detect molecules  
 CC derived from or indicative of pregnancy or of a disease, such as an  
 CC infectious, autoimmune or cancerous disease.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 3.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
 DB 1 QYIKANSKFIGITEL 15  
 |||||

RESULT 3  
 AAW11505 standard; Protein; 15 AA.

XX AAW11505;

XX 24-SEP-1997 (first entry)

DE Tetanus toxoid universal Th epitope TT830.

XX Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;  
 KW fusion protein; chimera; tetanus toxoid; helper T cell epitope;  
 KW antigen presentation; ds.  
 XX Clostridium tetani.

OS WO9640789-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09988.

XX 07-JUN-1995; 95US-0484172.

XX (MEDA-) MEDAREX INC.

PI Deo YM, Goldstein J, Graziano R, Somasundaram C;

XX WPI; 1997-052242/05.

DR N-PSDB; AAT58127.

XX Recombinant, multi-specific anti-Fc receptor antibody molecules -  
 PT also comprise an anti-target portion, used for the treatment of  
 PT cancer, autoimmune disease and pathogenic infection

XX Example 7; Fig 24; 115pp; English.

PS Synthetic DNA coding for the wild-type universal Th epitope from  
 CC tetanus toxoid, designated TT830, was fused to the 3'-end of DNA  
 CC encoding heavy chain sequences from the humanised anti-Fc gamma RI  
 CC monoclonal antibody H22. The resulting fusion protein was shown to  
 CC be significantly more efficient in antigen presentation and T cell  
 CC stimulation than the TT830 epitope alone. A similar fusion  
 CC construct was prepared coding for a mutant, antagonistic form of the  
 CC epitope (designated TT833S) fused to the anti-Fc gamma RI. The  
 CC Fab22-TT833S is at least 100 times more effective than TT833S in  
 CC inhibiting T cell activation.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 3.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
 DB 1 QYIKANSKFIGITEL 15  
 |||||

RESULT 4  
AAW67033  
ID AAW67033 standard; peptide; 15 AA.  
XX AC AAW67033;  
XX DT 15-DEC-1998 (first entry)  
XX DE Tetanus toxin fragment (residues 830-844).  
XX KW Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate;  
XX KW dendrimeric poly-lysine; epitope; tumour.  
XX OS Clostridium tetani.  
XX PN WO9843677-A1.  
08-OCT-1998.  
PF 27-MAR-1998; 98WO-EP01922.  
XX PR 27-MAR-1997; 97US-0041726.  
XX (INSP ) INST PASTEUR.  
XX PA Bay S, Cantacuzene D, Leclerc C, Lo-man R;  
XX PI WPI; 1998-557071/47.  
XX Carbohydrate peptide conjugate used as vaccine - comprises carrier  
XX PT with dendrimeric poly-lysine enabling multiple epitopes to be  
XX PT covalently attached  
XX PS Disclosure; Page 13; 55pp; English.  
XX The invention relates to a new carbohydrate peptide conjugate, which  
XX CC comprises a carrier with a dendrimeric poly-lysine enabling multiple  
XX CC epitopes to be covalently attached to it. Also claimed are: (1) an  
XX CC antibody purified from biological fluid or cells of organisms  
XX CC administered with the carbohydrate peptide conjugate, and (2) a diagnosis  
XX CC kit comprising antigen-specific antibodies elicited by immunisation with  
XX CC the carbohydrate peptide conjugate. The peptide conjugate, antibody and  
XX CC diagnosis kit are used to provide pharmaceutical compositions and  
XX CC vaccines against tumours. These can be used to support an immune response  
XX CC against viral infections caused by hepatitis virus, HIV or cytomegalo  
XX CC virus. They can be used to enhance immune responses, especially B- and T-  
XX CC cell responses, of humans and animals against bacterial infections. The  
XX CC carbohydrate peptide conjugate stimulates the antibody and T-cell  
XX CC response without stimulating undesired immune responses. The composition  
XX CC is capable of increasing the survival of tumour bearing humans and  
XX CC animals. The present sequence corresponds to residues 830-844 of tetanus  
XX CC toxin. The synthetic peptide corresponding to this sequence may be used  
XX CC as an epitope in a carbohydrate peptide conjugate.  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 74; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
|||||  
RESULT 5  
AAW71321  
ID AAW71321 standard; peptide; 15 AA.  
XX AC AAW71321;  
XX DT 26-NOV-1998 (first entry)

XX Universal helper T-cell epitope P2 derived from tetanus toxin.  
XX DE Liver stage; Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3;  
KW hepatic and erythrocytic stage protein; PyHEP17; vaccine;  
KW malaria parasite; teanus toxin; P2; helper T-cell epitope.  
XX Synthetic.  
OS Clostridium tetani.  
XX US5814617-A.  
XX 29-SEP-1998.  
XX 07-OCT-1994; 94US-0319704.  
XX 07-OCT-1994; 94US-0319704.  
XX (USNA ) US SEC OF NAVY.  
XX Charoenvit Y, Doolan DL, Hedstrom RC, Hoffman SL;  
XX WPI; 1998-541794/46.  
XX Vaccine for protecting mammal against infection by malaria caused by  
XX PT Plasmodium species - comprises a first nucleic acid encoding a first  
XX PT polypeptide capable of eliciting an immune reaction against an  
XX PT antigen expressed during the liver  
XX PS Disclosure; Column 12; 24pp; English.  
XX AAW71321-22 represent universal helper T-cell epitopes derived from  
XX CC tetanus toxin. They are used to enhance host immune response to  
XX CC vaccines. The specification describes a Plasmodium yoelii liver stage  
XX CC 17 kDa hepatic and erythrocytic stage protein designated PyHEP17. This  
XX CC protein elicits a response from an Igl monoclonal antibody designated  
XX CC Navy Yoelii Liver Stage 3 (NYLS3). This antibody does not recognise  
XX CC sporozoites, but does recognise P. yoelii liver stage parasites. NYLS3  
XX CC eliminates upto 90% of liver stage parasites. The specification  
XX CC describes a vaccine for reducing the severity or incidence of infection  
XX CC by a malaria parasite of the genus Plasmodium. The DNA vaccine comprises  
XX CC exon 1 and part of exon 2 of the PyHEP17 gene.  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 74; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
|||||  
RESULT 6  
AAW04051  
ID AAW04051 standard; peptide; 15 AA.  
XX AC AAW04051;  
XX 04-JAN-2000 (first entry)  
XX T-Helper epitope from tetanus toxoid.  
XX Covalently reactive antigen analog; CRAA; catalytic antibody;  
KW electrophilic reaction centre; phosphonate; boronate; vaccine;  
KW transition state analog; TSA; isostere; gp120; HIV-1; T-helper;  
KW tetanus; toxoid; B-T-epitope.  
XX Clostridium tetani.  
XX PN WO9948925-A1.  
XX

PD 30-SEP-1999.

XX 23-MAR-1999; 99WO-US06325.

XX 23-MAR-1998; 98US-0046373.

XX (UYNE-) UNIV NEBRASKA.

XX Paul S. Gololobov G. Smith L;

XX WPI; 1999-591076/50.

XX New covalently reactive antigen analogs used for treating e.g.  
PT autoimmune diseases, lymphoproliferative disorders, cancers, microbial  
PT infections, ischemic and reperfusion injury or septic shock.

XX Disclosure; Page 86; 158pp; English.

XX The patent discloses new covalently reactive antigen analogs (CRAA)  
CC of formula X1-Y-E-X2, in which X1 and X2 represent peptide sequences  
CC of an epitope of a disease-associated protein, Y is a positively  
CC charged amino acid residue, preferably Lys or Arg, and E is an  
CC electrophilic reaction centre, preferably a phosphonate or boronate  
CC moiety. Depending on the identity of the epitope, the CRAA may be used  
CC to stimulate production of catalytic antibodies specific for  
CC predetermined antigens associated with particular medical disorders.  
CC They may also be used to permanently inactivate endogenously produced  
CC catalytic antibodies produced in certain autoimmune diseases as well as  
CC in certain lymphoproliferative disorders.

CC Amongst the specifically exemplified CRAAs is one based on residues  
CC 421-436 of a B-cell epitope of gp120 (see AAY04046) which may be used  
CC to counter HIV-1 infections. When used as an immunogen, preferably this  
CC CRAA is conjugated at its N-terminal to a T-helper epitope from tetanus  
CC toxoid. The present sequence represents the T-helper epitope and  
CC corresponds to residues 830-844 of the toxoid.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

DB 1 QYIKANSKFIGITEL 15

RESULT 7

AAW67578

AAW67578 standard; peptide; 15 AA.

AAW67578;

XX 02-MAR-1999 (first entry)

XX T-cell epitope peptide #4 for chimeric fimbrin/T-cell epitope peptide.

XX Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;  
KW immunogenic composition; immune response.

XX Synthetic.

XX US5843464-A.

XX 01-DEC-1998.

XX 02-JUN-1995; 95US-0460502.

XX 02-JUN-1995; 95US-0460502.

XX (OHIS ) UNIV OHIO STATE.

XX Bakaletz LO, Kaumaya PTP;

XX

DR WPI; 1999-044514/04.

XX Synthetic chimeric fimbrin peptide - useful for vaccination against  
PT non-typable Haemophilus influenzae

XX Disclosure; Column 4; 16pp; English.

XX The invention relates to the manufacture of a synthetic chimeric peptide  
CC comprising a non-typable Haemophilus influenzae fimbrin peptide fused via  
CC a linker peptide to a T-cell epitope peptide. The chimeric peptide is  
CC used in immunogenic compositions which induce an immune response against  
CC non-typable Haemophilus influenzae. This sequence represents an example  
CC of a T-cell epitope peptide used to generate the chimeric peptide.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

DB 1 QYIKANSKFIGITEL 15

RESULT 8

AAW73220

ID AAW73220 standard; Protein; 15 AA.

XX AC AAW73220;

XX 25-JAN-1999 (first entry)

XX Tetanus toxoid epitope.

XX Multispecific single chain antibody; antibody H22; tumour cell; therapy;  
KW antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;  
KW epidermal growth factor receptor; breast cancer; ovarian cancer.

XX Synthetic.

XX US5837243-A.

XX 17-NOV-1998.

XX 07-JUN-1996; 96US-0661052.

XX 07-JUN-1996; 96US-0661052.

XX 07-JUN-1995; 95US-0484172.

XX (MEDA-) MEDAREX INC.

XX Deo YM, Goldstein J, Graziano R, Somasundaram C;

XX WPI; 1999-023374/02.

XX Specific killing of tumour cells - using a multi-specific molecule  
PT comprising an anti-Fc receptor antibody and a portion which binds to  
PT a target cell

XX Example 7; Column 27; 57pp; English.

XX This sequence represents a tetanus toxoid epitope and is recognised  
CC by the multispecific single chain antibody designated H22. The  
CC antibody can be used in the method of the invention for inducing  
CC antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell  
CC which is characterised by overexpression of HER 2/neu or epidermal growth  
CC factor receptor (EGFR), comprises contacting the tumour cell with a  
CC multispecific protein molecule (preferably a single chain antibody)  
CC comprising: (a) an anti-Fc receptor antibody or an antigen binding  
CC fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which  
CC binds to EGFR. The method can be used for treating cancers especially

CC breast cancer or ovarian cancer. The multispecific antibody can also  
CC be administered prophylactically to vaccinate a subject against infection  
CC by a target cell.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 20; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15

# RESULT 9

AAB4511  
AAB4511 standard; Protein; 15 AA.

AAB4511;

DT 26-FEB-2001 (first entry)

DE Tetanus P2 epitope SEQ ID NO: 23.

KW Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection;  
KW cancer; eosinophilia; vaccine; allergic rhinitis.

OS Clostridium tetani.

PN WO200065058-A1.

XX 02-NOV-2000.

PF 19-APR-2000; 2000WO-DK00205.

PR 23-APR-1999; 99DK-0000552.

PR 06-MAY-1999; 99US-0132811.

XX (MEBI-) M & E BIOTECH AS.

PA Klysner S;

XX WPI; 2000-672791/65.

DR Down-regulating interleukin 5 (IL-5) activity in humans by  
administering IL-5 and/or an IL-5 analogue, useful in the treatment,  
prophylaxis or amelioration of asthma or other chronic allergic  
conditions -

PS Example 1; Page 137; 172pp; English.

XX The present invention is concerned with methods of treating asthma,  
CC eosinophilia, allergic rhinitis and other allergic diseases. These  
CC involve the use of interleukin-5 (IL-5) analogues and modified IL-5  
CC proteins and their coding sequences to down-regulate IL-5 activity and  
CC thus reduce eosinophil numbers. The allergic diseases may be treated  
CC using autovaccines, nucleic acid vaccines or live vaccines. In addition,  
CC it is possible that they may be used in the treatment of cancer and  
CC helminthic infections.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15

# RESULT 10

AA82637

ID AAY82637 standard; peptide; 15 AA.

XX AC AAY82637;

XX DT 07-AUG-2000 (first entry)

XX Tetanus toxoid T cell epitope peptide SEQ ID NO:13.

DE T cell epitope; B cell epitope; allergy; allergen; antigenic;  
KW antiallergic; antiasthmatic; antiinflammatory; dermatological;  
KW immunosuppressive; vaccine; rhinitis; sinusitis; bronchial asthma;  
KW atopic dermatitis; acute urticaria; chronic urticaria;  
KW gastro-intestinal syndrome; food allergen; oro-pharyngeal syndrome;  
KW anaphylactic reaction; drug hypersensitivity; allergic reaction.

XX Clostridium tetani.

OS Synthetic.

XX WO200006694-A2.

XX 10-FEB-2000.

XX 20-JUL-1999; 99WO-BE00092.

XX 30-JUL-1998; 98EP-0870167.

XX (UNIO ) UCB SA.

XX Saint-Remy J, Jacquemin M;

XX WPI; 2000-422470/36.

XX New compound for prevention and treatment of allergies comprises at  
least one allergen antigenic determinant recognized by a B cell and at  
least one antigenic determinant which does not trigger T cell  
activation -

XX Example 6; Page 30; 50pp; English.

XX The present invention describes a compound (I) for the prevention and/or  
treatment of allergy. The compound comprises at least one allergen  
antigenic determinant (i) recognised by a B cell or an antibody secreted  
by a B cell of a non-atopic individual and at least one antigenic  
determinant (ii) different from the allergen that triggers T cell  
activation. (I) has antiallergic, antiasthmatic, antiinflammatory,  
CC dermatological and immunosuppressive activities, and can be used in a  
CC vaccine. (I) may be used in a pharmaceutical or cosmetic medicament to  
CC treat and/or prevent allergies or a disease of allergic origin,  
CC especially hypersensitivities. These include rhinitis, sinusitis,  
CC bronchial asthma, atopic dermatitis, some forms of acute and chronic  
CC urticaria, gastro-intestinal syndromes associated with the ingestion of  
CC food allergens, oro-pharyngeal syndrome, anaphylactic reactions  
CC associated with drug hypersensitivities and/or a mixture of these. The  
CC use of (I) in the treatment of allergic conditions avoids the need for  
CC drug treatment, which often causes undesirable side-effects. Also, prior  
CC art drug therapies alleviate symptoms, but do not influence their  
CC causes, however (I) actually combats the cause of an allergic reaction.  
CC The present sequence represents a peptide, which is used in an  
CC example from the present invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15

# RESULT 11

AA92625  
ID AAY92625 standard; Protein; 15 AA.  
XX  
AC AAY92625;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Foreign epitope P2.  
XX  
KW Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2;  
KW Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination;  
KW cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer;  
KW prostate cancer; cell-associated peptide antigen.  
XX  
OS Clostridium tetani.  
XX  
PN WO200020027-A2.  
XX  
PD 13-APR-2000.  
XX  
DE 05-OCT-1999; 99WO-DK00525.  
XX  
DE 05-OCT-1998; 98DK-0001261.  
XX  
PD 20-OCT-1998; 98US-0105011.  
XX  
PA (MEBI-) M & E BIOTECH AS.  
XX  
PI Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
PI Gautam A, Birk P, Karlsson G;  
XX  
DR WPI; 2000-349917/30.  
DR N-PSDB; AAA09460.  
XX  
XX Inducing immune responses to weakly immunogenic, tumor associated  
XX peptide antigens for the treatment of breast and prostate cancer  
XX  
PS Example 1; Page 213; 220pp; English.  
XX  
CC The claims detail a method for inducing immune responses against weakly  
CC immunogenic cell-associated peptide antigens (PA) such as those  
CC associated with cancers (i.e. self-proteins), for example, human  
CC prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or  
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting  
CC simultaneous presentation by antigen producing cells (APCs) of the  
CC animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)  
CC group derived from the PA and/or at least 1 B-cell group derived from the  
CC cell-associated PA; and (2) at least 1 first T helper cell group which is  
CC foreign to the animal. Analogues of human PSM, human Her2 and  
CC human/murine FGF8b comprising a substantial part of all known and  
CC predicted CTL and B-cell epitopes of the respective PA and including at  
CC least one foreign T helper epitope (e.g. P2 and/or P30) are also claimed.  
CC The method is used to treat prostate, prostate/breast or breast cancer  
CC when the PA is human PSM, FGF8b and Her2, respectively.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 100.0%; Score 74; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
RESULT 12  
AAY84427  
ID AAY84427 standard; Peptide; 15 AA.  
XX  
AC AAY84427;  
XX  
DT 25-JUL-2000 (first entry)  
XX

Amino acid sequence of the tetanus toxoid P2 epitope.  
Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;  
tumour necrosis factor receptor; type II transmembrane protein;  
osteoclast differentiation; CSF-1; osteoclast activator;  
immune response; osteoporosis; bone resorption;  
tetanus toxoid P2 epitope.  
Clostridium tetani.  
WO200015807-A1.  
23-MAR-2000.  
13-SEP-1999; 99WO-DK00481.  
15-SEP-1998; 98DK-0001164.  
02-OCT-1998; 98US-0102896.  
(MEBI-) M & E BIOTECH AS.  
Halkier T, Haaning J;  
WPI; 2000-271444/23.  
In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used  
to treat, prevent and ameliorate osteoporosis -  
Example; Page 106; 110pp; English.  
The present sequence represents the tetanus toxoid P2 epitope. It is  
used to create a fusion protein with murine osteoprotegerin ligand  
(OPGL). Osteoprotegerin is a secreted member of the tumour necrosis  
factor receptor family, which blocks osteoclastogenesis in a dose  
dependent manner. The OPGL protein is synthesised as a type II  
transmembrane protein. The murine and human OPGL polypeptides are 87%  
homologous. OPGL is a potent osteoclast differentiation factor when  
combined with CSF-1. It is not capable of inducing osteoclast  
differentiation in the absence of CSF-1. OPGL is also an activator of  
mature osteoclasts. The specification describes a method for the in vivo  
down-regulation of OPGL activity in an animal. The method comprises  
using at least one OPGL polypeptide or subsequence, and/or at least one  
OPGL analogue to induce an immune response in the animal. The method  
and OPGL polypeptide are useful for treating, preventing and ameliorating  
osteoporosis or other diseases or conditions characterised by excessive  
bone resorption.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 100.0%; Score 74; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
RESULT 13  
AAY70300  
ID AAY70300 standard; peptide; 15 AA.  
XX  
AC AAY70300;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Clostridium tetani tetanus toxoid T-cell epitope, P589.  
XX  
KW Recombinant protein; CDC/NIH/VAC-1; multivalent; malaria; vaccine;  
KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;  
KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;  
KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1;  
KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;

KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
 KW Pfg27; antiparasitic; prevention; anti-CDC/NIIH/VAC-1 antibody.

XX Clostridium tetani.

XX WO200011179-A1.

XX 02-MAR-2000.

XX 19-AUG-1999; 99WO-US18869.

XX 21-AUG-1998; 98US-0097703.

XX (NATM-) NAT INST IMMUNOLOGY.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Lal AA, Shi YP, Hasnain SE;

XX WPI; 2000-237654/20.

XX Novel recombinant protein as vaccine for treating malarial infection  
 PT comprises antigenic peptides obtained from different stages of  
 PT plasmodium falciparum life cycle

PS Claim 2; Page 17; 52pp; English.

XX The present sequence is the tetanus toxoid T-cell epitope p589, derived  
 CC from Clostridium tetani. It is used in the construction of recombinant  
 CC protein CDC/NIIH/VAC-1, which is a multivalent, multistage malarial  
 CC vaccine. The recombinant protein comprises, melittin signal peptide,  
 CC (His)6 tag. T-cell epitope from tetanus toxoid and 21 antigenic epitopes  
 CC from circumsporozoite protein (CSP), sporozoite surface protein-2  
 CC (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1  
 CC (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding  
 CC antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete  
 CC specific antigen, Pfg27. These epitopes were obtained at different stages  
 CC of the life cycle of P. falciparum. CDC/NIIH/VAC-1 vaccine has  
 CC antiparasitic activity and can be used for treatment and prevention of  
 CC malarial infections. Anti-CDC/NIIH/VAC-1 antibodies can be used for  
 CC detecting P. falciparum in biological samples.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;

1 QYIKANSKFIGITEL 15  
 |||||  
 1 QYIKANSKFIGITEL 15

RESULT 14

AA44763

ID AAY44763 standard; peptide; 15 AA.

XX AAY44763;

XX 04-MAY-2000 (first entry)

XX Tetanus toxoid protein derived T-cell activating epitope P2.

XX Surface layer protein; S-layer secretion signal; antibiotic; vaccine;  
 KW recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff;  
 KW antibacterial enzyme; surface glycoprotein; T-cell activating epitope;  
 KW P2; tetanus toxoid; IPNV; Infectious pancreatic necrosis virus.

XX Clostridium tetani.

XX WO200004170-A1.

XX 27-JAN-2000.

PF 14-JUL-1999; 99WO-CA00637.

XX 14-JUL-1998; 98CA-2237704.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Smit J;

XX WPI; 2000-182434/16.

XX Cleavage of Caulobacter produced recombinant fusion proteins useful for  
 PT producing vaccine peptides

XX Example 2; Page 16; 33pp; English.

XX The patent discloses a method for cleaving a recombinant fusion protein  
 CC which is produced by Caulobacter and consists of Caulobacter surface  
 CC layer (S-layer) protein (containing the C-terminal secretion signal) and  
 CC a target protein heterologous to Caulobacter. The cleavage of target  
 CC protein from the S-layer protein is carried out under mild acid  
 CC conditions so that cleavage occurs at aspartate-proline dipeptide site  
 CC without solubilising the protein. The cleavage is accomplished while the  
 CC fusion protein is in an insoluble aggregate form which facilitates  
 CC purification of the protein. The method is useful for producing pure  
 CC proteins including recombinant human and animal therapeutic antibiotic  
 CC and vaccine peptides, enzymes, protein polymers, and antibacterial  
 CC enzymes for foodstuffs.

XX The present sequence is a T-cell activating epitope P2 derived  
 CC from tetanus toxoid protein. This sequence was fused to a DNA encoding  
 CC a fragment of infectious pancreatic necrosis virus surface glycoprotein  
 CC which is a vaccine candidate. This chimeric protein was in turn fused to  
 CC DNA encoding C. crescentus S-layer secretion signal (corresponds to the  
 CC C-terminal portion of the S-layer protein from amino acid 690 onwards and  
 CC contains native Asp-Pro site) for construction of a recombinant  
 CC fusion construct which is expressed in Caulobacter and then cleaved  
 CC to recover the vaccine candidate protein.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;

1 QYIKANSKFIGITEL 15  
 |||||  
 1 QYIKANSKFIGITEL 15

RESULT 15

AAE11763

ID AAE11763 standard; peptide; 15 AA.

XX AAE11763;

XX 18-DEC-2001 (first entry)

XX Clostridium tetani P2 epitope.

XX Amyloid protein; neuroprotective; nootropic; immunostimulant; vaccine;  
 KW Alzheimer's disease; anticonvulsant; gene therapy; Pick's disease;  
 KW antidiabetic; systemic amyloidosis; maturity onset diabetes; ALS;  
 KW amyotrophic lateral sclerosis; Parkinson's disease; encephalopathy;  
 KW Huntington's disease; fronto-temporal dementia; P2 epitope.

XX Clostridium tetani.

XX WO200162284-A2.

XX 30-AUG-2001.

XX 19-FEB-2001; 2001WO-DK00113.

XX 21-FEB-2000; 2000DK-0000265.

```

PR 01-MAR-2000; 2000US-186295P.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Birk P, Jensen MR, Nielsen KG;
XX
XX WPI; 2001-589796/66.
XX N-PSDB; AAD18755.
XX
XX In vivo down-regulation of amyloid protein for the treatment of
PT Alzheimer's, comprises presenting an amyloidogenic polypeptide or its
PT subsequence and/or at least one analogue of the amyloidogenic
PT polypeptide to the immune system
XX
XX Example 3; Page 117; 120pp; English.
XX
XX The invention relates to a method for in vivo down-regulation of amyloid
CC protein such as beta amyloid (Abeta) in an animal, including human. The
CC method comprising presenting to the animal's immune system an
CC immunogenically effective amount of at least one amyloidogenic protein
CC or its subsequence and/or at least one analogue of the amyloidogenic
CC polypeptide. The amyloidogenic protein or its subsequence, and its
CC analogue is useful for the preparation of an immunogenic composition
CC comprising an adjuvant for down-regulating amyloid in an animal. They are
CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's
CC disease or other diseases characterised by amyloid deposits. They are
CC also useful in the treatment of systemic amyloidosis, maturity onset
CC diabetes, Parkinson's disease, Huntington's disease, fronto-temporal
CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and
CC prion-related transmissible spongiform encephalopathies. They are also
CC useful for inducing production of antibodies against an amyloidogenic
CC polypeptide. The present sequence is Clostridium tetani P2 epitope
CC related to the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 100.0%; Score 74; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 OYIKANSKFIGITEL 15
DB 1 OYIKANSKFIGITEL 15

```

Search completed: October 10, 2002, 16:00:56  
Job time : 5.02108 secs



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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 1.76205 Seconds  
(without alignments)  
329.613 Million cell updates/sec

Title: US-09-787-126-34  
Perfect score: 74  
Sequence: 1 QVIKANSRFIGITEL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	1314	1 TETX_CLOTE	P04958 clostridium
2	44	59.5	66	1 VGB4_BPML5	Q05301 mycobacteri
3	42.5	57.4	1682	1 MSP1_PLAF3	P19598 plasmodium
4	42.5	57.4	1701	1 MSP1_PLAF5	P13819 plasmodium
5	42.5	57.4	1701	1 MSP1_PLAFM	P08569 plasmodium
6	42.5	57.4	1726	1 MSP1_PLAFC	P04934 plasmodium
7	42.5	57.4	1726	1 MSP1_PLAFC	P04934 plasmodium
8	41	55.4	204	1 PYRC_SERMA	Q9S3S1 serratia ma
9	41	55.4	899	1 V120_HSVSA	Q01055 herpesvirus
10	40	54.1	194	1 ACPD_HAEIN	P43013 haemophilus
11	40	54.1	601	1 PEPF_LACLC	P54124 lactococcus
12	40	54.1	601	1 PEPF_LACLC	Q9CEV7 lactococcus
13	40	54.1	644	1 YHJ9_YEAST	P38694 saccharomyc
14	39	52.7	213	1 RAD_MYCCA	P10251 mycoplasma
15	38	51.4	256	1 YD83_METJA	Q58778 methanococc
16	38	51.4	287	1 TRUB_AQUAE	Q66922 aquifex aeo
17	38	51.4	572	1 HEMA_PI3HT	P12562 human parai
18	37	50.0	191	1 Y096_HAEIN	P43940 haemophilus
19	37	50.0	445	1 GNT1_HUMAN	P26572 homo sapien
20	37	50.0	447	1 GNT1_MOUSE	P27808 mus musculu
21	37	50.0	447	1 GNT1_MOUSE	P27115 oryctolagus
22	37	50.0	447	1 GNT1_MOUSE	Q09325 rattus norv
23	37	50.0	490	1 Y032_BORBU	Q51063 borrelia bu
24	37	50.0	510	1 G6PD_ASPNG	P48826 aspergillus
25	37	50.0	511	1 G6PD_ASPNG	P41764 emericella
26	37	50.0	548	1 YDD2_SCHPO	Q10428 schizosacch
27	36	48.6	169	1 Y358_BUCAI	P57439 buchnera ap
28	36	48.6	258	1 MIP_CHLPN	Q9Z7P3 chlamydia p
29	36	48.6	296	1 YD01_CLOAB	P33659 clostridium
30	36	48.6	333	1 DPOB_XENLA	Q57383 xenopus lae
31	36	48.6	451	1 MORD_BACSU	Q03522 bacillus su
32	36	48.6	461	1 NIFN_RHOCA	P19077 rhodobacter
33	36	48.6	495	1 G6PD_PICJA	P11410 picchia jadi

34	36	48.6	530	1 YND1_YEAST	P40009 saccharomyc
35	36	48.6	774	1 RRP3_INCBE	P21770 influenza c
36	36	48.6	774	1 RRP3_INCBE	P13877 influenza c
37	36	48.6	1630	1 MSP1_PLAFK	P04932 plasmodium
38	36	48.6	1639	1 MSP1_PLAFW	P04933 plasmodium
39	35	47.3	176	1 NUGC_SPIOL	Q9M318 spinacia ol
40	35	47.3	261	1 CABV_CHICK	P04354 gallus gall
41	35	47.3	294	1 CDD_ECOLI	P13652 schischerichia
42	35	47.3	321	1 YDG7_SCHPO	Q10494 schizosacch
43	35	47.3	329	1 DHOA_EMENI	P25415 emericella
44	35	47.3	353	1 4LKD_LACHE	P17212 lactobacill
45	35	47.3	402	1 VGLD_HVEA	P24872 equine herp

## ALIGNMENTS

RESULT 1  
TETX\_CLOTE  
ID TETX\_CLOTE STANDARD; PRT; 1314 AA.  
AC P04958;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 13-JUL-1999 (Rel. 38, Last annotation update)  
DE Tetanus toxin precursor (EC 3.4.24.68) (Pentoxylisin).  
OS Clostridium tetani.  
OG Plasmid.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1513;  
RN [1]  
RP MEDLINE=87053814; PubMed=3536478;  
RA Elsel U., Jarausch W., Goretzki K., Henschen A., Engels J.,  
RA Weller U., Hudel M., Habermann E., Niemann H.:  
RT "Tetanus toxin: Primary structure, expression in E. coli, and  
RT homology with botulinum toxins.";  
RL EMBO J. 5:2495-2502(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CN3911;  
RA Fairweather N.F., Lyness V.A.;  
RT "The complete nucleotide sequence of tetanus toxin.";  
RL Nucleic Acids Res. 14:7809-7812(1986).  
RN [3]  
RP SEQUENCE OF 742-1314 FROM N.A.  
RX MEDLINE=86085672; PubMed=3510187;  
RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;  
RT "Cloning, nucleotide sequencing, and expression of tetanus toxin  
fragment C in Escherichia coli.";  
RL J. Bacteriol. 165:21-27(1986).  
RN [4]  
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.  
RX MEDLINE=90201034; PubMed=2108021;  
RA Krieglstein K., Henschen A., Weller U., Habermann E.;  
RT "Arrangement of disulfide bridges and positions of sulfhydryl groups  
in tetanus toxin.";  
RL Eur. J. Biochem. 188:39-45(1990).  
RN [5]  
RP PARTIAL SEQUENCE.  
RX MEDLINE=92037649; PubMed=1935979;  
RA Krieglstein K.G., Henschen A.H., Weller U., Habermann E.;  
RT "Limited proteolysis of tetanus toxin. Relation to activity and  
identification of cleavage sites.";  
RL Eur. J. Biochem. 202:41-51(1991).  
RN [6]  
RP IDENTIFICATION AS ZINC-PROTEASE.  
RX MEDLINE=93010948; PubMed=1396558;  
RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,  
RA Montecucco C.;  
RT "Tetanus toxin is a zinc protein and its inhibition of  
RT neurotransmitter release and protease activity depend on zinc.";

EMBO J. 11:3577-3583(1992).  
[7]  
RP IDENTIFICATION OF SUBSTRATE.  
RX MEDLINE-93063293; PubMed-1331807;  
RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,  
RT Dasgupta B.R., Montecucco C.;  
"Tetanus and botulinum-B neurotoxins block neurotransmitter release  
by proteolytic cleavage of synaptobrevin.";  
RL Nature 359:832-835(1992).  
[8]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.  
RX MEDLINE-97475217; PubMed-9334741;  
RA Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,  
Sax M.;  
"Structure of the receptor binding fragment HC of tetanus  
neurotoxin.";  
RL Nat. Struct. Biol. 4:788-792(1997).  
CC -!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER  
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED  
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD  
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT  
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC  
ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-1-PHE-77  
BOND OF SYNAPTOSOMAL VESICLES.  
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-1-PHE-77 BOND IN  
SYNAPTOSOMAL VESICLES.  
CC -!- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO  
YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE  
AND ARE NON-TOXIC AFTER SEPARATION.  
CC -!- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO  
GANGLIOSIDE RECEPTORS.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.  
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CC  
CC EMBL; X04436; CAA28033.1; -  
CC EMBL; M12739; AAA23282.1; -  
CC EMBL; X06214; CAA29564.1; -  
CC PIR; A25689; BTCLTN.  
CC PDB; 1AF9; 29-APR-98.  
CC PDB; 1A8D; 14-OCT-98.  
CC MEROPS; M27.001; -  
CC InterPro; IPR000395; Bontoxilysin.  
CC InterPro; IPR000130; Zn\_Mtpeptidse.  
CC Pfam; PF01742; Peptidase\_M27; 1.  
CC PRINTS; PR00760; BONTOXILYSIN.  
CC ProDom; PD001963; Bontoxilysin; 1.  
CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;  
KW 3D-structure.  
FT INIT MET 0 0  
FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.  
FT CHAIN 457 1314 TETANUS TOXIN HEAVY CHAIN.  
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 233 233 BY SIMILARITY.  
FT METAL 236 236 ZINC (CATALYTIC) (BY SIMILARITY).  
FT TRANSMEM 226 246 POTENTIAL.  
FT TRANSMEM 669 689 POTENTIAL.  
FT DISULFID 438 466 INTERCHAIN.  
FT DISULFID 1076 1092  
SQ SEQUENCE 1314 AA; 150550 MW; 134C3657133EF8D CRC64;  
Query Match 100.0%; Score 74; DB 1; Length 1314;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15

Db 829 QYIKANSKFIGITEL 843  
RESULT 2  
VG84\_BPML5  
ID VG84\_BPML5 STANDARD; PRT; 66 AA.  
AC Q05301;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Gene 84 protein (GP84).  
GN 84.  
OS Mycobacteriophage L5.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=31757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-93211289; PubMed-8459766;  
RA Hatfull G.F., Sarkis G.J.;  
"DNA sequence, structure and gene expression of mycobacteriophage L5:  
a phage system for mycobacterial genetics.";  
RT Mol. Microbiol. 7:395-405(1993).  
CC  
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CC  
CC EMBL; Z18946; CAA79460.1; -  
CC PIR; S31029; S31029.  
SQ SEQUENCE 66 AA; 7424 MW; 9C7104C7A4FA74A5 CRC64;  
Query Match 59.5%; Score 44; DB 1; Length 66;  
Best Local Similarity 57.1%; Pred. No. 0.21;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 YIKANSKFIGITEL 15  
Db 50 YIKRNGKFGVTWEV 63  
RESULT 3  
MSP1\_PLAF3  
ID MSP1\_PLAF3 STANDARD; PRT; 1682 AA.  
AC P19598; Q25921;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)  
DE (PMMSA) (P190).  
GN MSP-1.  
OS Plasmodium falciparum (isolate ro-33 / Ghana).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5834;  
RN [1]  
RP SEQUENCE OF 1-1061 FROM N.A.  
RX MEDLINE-88166657; PubMed-3327688;  
RA Certa U., Rotmann D., Matile H., Reber-Liske R.;  
"A naturally occurring gene encoding the major surface antigen  
precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";  
RL EMBO J. 6:4137-4142(1987).  
RN [2]  
RP SEQUENCE OF 1032-1682 FROM N.A.  
RX MEDLINE-95354793; PubMed-7628566;  
RA Tolle R., Bujard H., Cooper J.A.;  
"Plasmodium falciparum: variations within the C-terminal region of  
merozoite surface antigen-1.";  
RL Exp. Parasitol. 81:47-54(1995).  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor



(Potential).

-1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.

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-----

EMBL; X05624; CAA29112.1; --  
 PIR; A26868; A26868.  
 PIR; B25120; B25120.  
 InterPro; IPR000561; EGF-like.  
 Pfam; PF00008; EGF; 1.  
 Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
 Transmembrane; GPI-anchor.

CHAIN 1 19  
 SIGNAL 1 19  
 FT CHAIN 20 1701 MEROZOITE SURFACE PROTEIN 1.  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 470 470 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 536 536 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 802 802 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 899 899 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 919 919 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 965 965 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 991 991 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1196 1196 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1588 1588 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 1701 AA; 193768 MW; 3FC2EC59AF96EA98 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1701;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 OYIKANSKFI-GITE 14  
 I:::||||| I::|

Db 1001 QFVKSNSKVIITGLTE 1015

RESULT 6

MSPL\_PLAFC STANDARD; PRT; 1726 AA.  
 AC P04934;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Merozoite surface protein 1 precursor (Merozoite surface antigens)  
 DE (PMWSA) (P195).  
 GN MSP-1.  
 OS Plasmodium falciparum (isolate Camp / Malaysia).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5835;  
 RN [1]  
 RP SEQUENCE OF 1-1103 FROM N.A.  
 RX MEDLINE=86205236; PubMed=3517809;  
 RA Weber J.L., Leininger W.M., Lyon J.A.;  
 RT "Variation in the gene encoding a major merozoite surface antigen of the human malaria parasite Plasmodium falciparum.";  
 RT Nucleic Acids Res. 14:3311-3323(1986).  
 RN [2]  
 RP SEQUENCE OF 1104-1726 FROM N.A.  
 RX MEDLINE=88143999; PubMed=3278296;  
 RA Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;  
 RT "Merozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum.";  
 RT Nucleic Acids Res. 16:1206-1206(1988).

-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (potential).

-1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.

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-----

EMBL; X03831; CAA27446.1; --  
 PIR; A23386; SAZQM.  
 InterPro; IPR000561; EGF-like.  
 Pfam; PF00008; EGF; 1.  
 Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
 Transmembrane; GPI-anchor.

CHAIN 1 19  
 SIGNAL 1 19  
 FT CHAIN 20 1726 MEROZOITE SURFACE PROTEIN 1.  
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 924 924 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 944 944 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 990 990 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1114 1114 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 1726 AA; 196197 MW; DD8AD45FA352BCF3 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1726;  
 Best Local Similarity 60.0%; Pred. No. 12;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 OYIKANSKFI-GITE 14  
 I:::||||| I::|

Db 1026 QFVKSNSKVIITGLTE 1040

RESULT 7

MSPL\_PLAFC STANDARD; PRT; 1726 AA.  
 AC P50495;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Merozoite surface protein 1 precursor (Merozoite surface antigens)  
 DE (PMWSA) (P195).  
 GN MSP-1.  
 OS Plasmodium falciparum (isolate Palo Alto / Uganda).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=57270;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89005525; PubMed=3049134;  
 RA Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,  
 RA Siddiqui W.A.;  
 RT "Plasmodium falciparum: gene structure and hydropathy profile of the major merozoite surface antigen (gp195) of the Uganda-Palo Alto isolate.";  
 RT Exp. Parasitol. 67:1-11(1988).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (potential).  
 CC -1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.

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CC EMBL; M37213; AAA29611.1; -  
 CC InterPro; IPR000561; EGF-like.  
 CC Pfam; PF00008; EGF; 1.

CC Malaria; Merzoite; Polyprotein; Repeat; Signal; Glycoprotein;  
 CC Transmembrane; GPI-anchor.

FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 1726 MERZOITE SURFACE PROTEIN 1.  
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 827 827 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 924 924 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 944 944 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 990 990 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1114 1114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1726 AA; 196174 MW; 5B59CEFA2F9A026 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1726;  
 Best Local Similarity 60.0%; Pred. No. 12;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 QYKANSKFI-GITE 14  
 DB 1026 QFVKSNSKVIQLTE 1040  
 I:::|::| |::|

RESULT 8  
 ID PYRC\_SERMA STANDARD; PRT; 204 AA.  
 AC Q9S3L1.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Dihydroorotase (EC 3.5.2.3) (DHOase) (Fragment).  
 GN PYRC.  
 OS Serratia marcescens.  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Serratia.  
 OX NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SM6;  
 RA Berkmen M.; Benedik M.J.;  
 RT "DnaI inhibits transcription of Serratia marcescens nuclease."  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O -> N-carbamoyl-L-  
 CC aspartate.  
 CC -1- COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH  
 CC IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO  
 CC TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY  
 CC SIMILARITY).  
 CC -1- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 1.

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CC EMBL; AF175466; AAD50307.1; ALT\_INIT.  
 CC InterPro; IPR002195; Dihydroorotase.  
 CC PROSITE; PS00482; DIHYDROOROTASE\_1; PARTIAL.  
 CC PROSITE; PS00483; DIHYDROOROTASE\_2; 1.  
 CC Pyrimidine biosynthesis; Hydrolase; Zinc.  
 FT NON\_TER 1  
 SQ SEQUENCE 204 AA; 22899 MW; 9DB0B6C9B834B310 CRC64;

Query Match 55.4%; Score 41; DB 1; Length 204;  
 Best Local Similarity 46.2%; Pred. No. 2.4;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 QYKANSKFI-GITE 13  
 DB 42 QYVQAGNREFGAT 54  
 I:::|::| |::|

RESULT 9  
 ID V120\_HSVSA STANDARD; PRT; 899 AA.  
 AC Q01055;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Capsid assembly protein 63.  
 GN 63 OR EERF1.  
 OS Herpesvirus saimiri (strain 11).  
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Gammaherpesvirinae; Rhadinovirus.  
 OX NCBI\_TaxID=10383;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92333688; PubMed-1321287;  
 RA Albrecht J.-C.; Nicholas J.; Biller D.; Cameron K.R.; Biesinger B.;  
 RA Newman C.; Wittmann S.; Craxton M.A.; Coleman H.; Fleckenstein B.;  
 RA Honess R.W.;  
 RT "Primary structure of the herpesvirus saimiri genome."  
 RL J. Virol. 66:5047-5058(1992).

CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,  
 CC EBV-1 23, EBV BOLF1, VZV 21, HVS-1 63, AND HCMV UL47.  
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CC EMBL; X64346; CAA45686.1; -  
 CC EMBL; M86409; AAA46139.1; -  
 CC PIR; G36812; G36812.  
 KW Capsid assembly.  
 SQ SEQUENCE 899 AA; 103350 MW; F1429B3770A2885E CRC64;  
 Query Match 55.4%; Score 41; DB 1; Length 899;  
 Best Local Similarity 50.0%; Pred. No. 11;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 QYKANSKFI-GITE 14  
 I:::|::| |::|

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Db 124 QYTSNATFTGLSE 137
RESULT 10
ACPD_HAEIN STANDARD; PRT; 194 AA.
AC P43013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP
DE phosphodiesterase).
GN ACPD OR H11366.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=96186898; PubMed=8635745;
Chandler M.S., Smith R.A.;
"Characterization of the Haemophilus influenzae topA locus: DNA
topoisomerase I is required for genetic competence.";
RL Gene 169:25-31(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: CONVERTS HOLO-ACP TO APO-ACP BY HYDROLYTIC CLEAVAGE OF
CC THE PHOSPHOPANTHEINE RESIDUE FROM ACP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: [Acyl-carrier protein] + H(2)O -> 4'-
CC phosphopantetheine + apoprotein.
CC -1- SIMILARITY: BELONGS TO THE ACPD FAMILY.
CC -----
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CC -----
DR EMBL; U20964; AAC43728.1; -
DR EMBL; U32816; AAC23013.1; -
DR TIGR; H11366; -
KW Hydrolase; Complete proteome.
SQ SEQUENCE 194 AA; 21208 MW; A8AEC9D00829522C CRC64;

Query Match 54.1%; Score 40; DB 1; Length 194;
Best Local Similarity 53.3%; Pred. No. 3.5;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QYKANSKFIGITEL 15
Db 147 QYKRSILGFIGITDV 161
RESULT 11
PEFL_LACLC
ID PEFL_LACLC STANDARD; PRT; 601 AA.

Query Match 54.1%; Score 40; DB 1; Length 601;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYKANSKFIGITEL 15
Db 284 RYELRKKILGIDTL 298
RESULT 12
PEPF_LACLA
ID PEPF_LACLA STANDARD; PRT; 601 AA.
AC Q9CEV7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Oligoendopeptidase F homolog (EC 3.4.24.-).
GN PEPF OR L11727.

```

OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Lactococcus.  
 OX NCBI\_TaxID=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IL1403;  
 RX MEDLINE=21235186; PubMed=11337471;  
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
 RT lactis ssp. lactis IL1403";  
 RL Genome Res. 11:731-753(2001).  
 CC -1- FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO  
 CC ACIDS WITH A RATHER WIDE SPECIFICITY (BY SIMILARITY).  
 CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.  
 CC -----  
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 CC -----  
 CC EMBL: AE006403; AAK05825.1;  
 CC InterPro: IPR001567; Peptidase\_M3.  
 CC InterPro: IPR000130; Zn\_MTPeptidase.  
 CC Pfam: PF01432; Peptidase\_M3; 1.  
 CC PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 CC Hydrolase; Metalloprotease; Zinc; Complete proteome.  
 CC METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).  
 CC ACT\_SITE 388 388 BY SIMILARITY.  
 CC METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).  
 CC METAL 394 394 ZINC (CATALYTIC) (BY SIMILARITY).  
 CC SEQUENCE 601 AA; 69883 MW; 045E6873F10FE19A CRC64;  
 CC -----  
 CC Query Match 54.1%; Score 40; DB 1; Length 601;  
 CC Best Local Similarity 46.7%; Pred. No. 11;  
 CC Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 CC -----  
 CC RESULT 13  
 CC YHJ9\_YEAST STANDARD; PRT; 644 AA.  
 CC AC P38694;  
 CC DT 01-FEB-1995 (Rel. 31, Created)  
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Hypothetical aldehyde-dehydrogenase like protein in FIL1-VMA10  
 CC DE intergenic region.  
 CC GN YH039C.  
 CC OS Saccharomyces cerevisiae (Baker's yeast).  
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CC OX NCBI\_TaxID=4932;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=S288C / AB972;  
 CC RX MEDLINE=94378003; PubMed=8091229;  
 CC RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
 CC Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,  
 CC Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
 CC Latrelle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,  
 CC Nham M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,  
 CC Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
 CC Vaudin M.;  
 CC "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome

VIII.";  
 RL Science 265:2077-2082(1994).  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U00062; AAB68915.1;  
 CC PIR: S46746; S46746.  
 CC SGD: S0001081; YHR039C.  
 CC InterPro: IPR002086; Aldehyde\_dehydr.  
 CC Pfam: PF00171; aldehyd; 1.  
 CC PROSITE: PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 CC PROSITE: PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 CC KW Hypothetical protein; Oxidoreductase.  
 CC FT ACT\_SITE 354 354 BY SIMILARITY.  
 CC FT ACT\_SITE 389 389 BY SIMILARITY.  
 CC SEQUENCE 644 AA; 71320 MW; 54DADDAEB2A16D4D CRC64;  
 CC -----  
 CC Query Match 54.1%; Score 40; DB 1; Length 644;  
 CC Best Local Similarity 50.0%; Pred. No. 12;  
 CC Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 CC -----  
 CC QY 1 QYIKANSKFGITEL 15  
 CC DB 38 QIIQDNQKLGITTL 52  
 CC -----  
 CC RESULT 14  
 CC KAD\_MYCCA STANDARD; PRT; 213 AA.  
 CC ID KAD\_MYCCA  
 CC AC P10251;  
 CC DT 01-MAR-1989 (Rel. 10, Created)  
 CC DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
 CC GN ADK.  
 CC OS Mycoplasma capricolum.  
 CC OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 CC OC Entomoplasmataceae.  
 CC OX NCBI\_TaxID=2095;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=ATCC 27343 / K1D;  
 CC RX MEDLINE=88142549; PubMed=3481422;  
 CC RA Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;  
 CC "The ribosomal protein gene cluster of Mycoplasma capricolum.";  
 CC Mol. Gen. Genet. 210:314-322(1987).  
 CC CC -1- FUNCTION: THIS SMALL UBQUITOUS ENZYME IS ESSENTIAL FOR  
 CC MAINTENANCE AND CELL GROWTH.  
 CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X06414; CAA29724.1;  
 CC PIR: S02851; K1VNC.  
 CC HSP: P27142; IZIN.  
 CC InterPro: IPR000850; Adenylate\_kin.  
 CC Pfam: PF00406; adenylatekinase; 1.  
 CC DR



Job time : 4.76205 secs

```
DR PRINTS; PR00094; ADENYLTKINASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW .Transferase; Kinase; ATP-binding.
FT NP_BIND 7 15 ATP (BY SIMILARITY).
SQ SEQUENCE 213 AA; 24616 MW; FBCFA426B6F92E16 CRC64;

Query Match          52.7%; Score 39; DB 1; Length 213;
Best Local Similarity 72.7%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YIKANSKEFIGI 12
DB 183 YFKTNSKFEI 193

RESULT 15
YD83_METJA STANDARD; PRT; 256 AA.
AC Q58778;
DT 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1383 precursor.
GN MJ1383.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geophagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: TO M.JANNASCHII MJ0761.
CC -----
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CC -----
CC EMBL; U67578; AAB99393.1;
CC TIGR; MJ1383;
CC InterPro; IPR001130; TatD.
CC Pfam; PF01026; TatD_DNase; 1.
CC KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 256 HYPOTHETICAL PROTEIN MJ1383.
SQ SEQUENCE 256 AA; 29036 MW; 6D26F427EAB54675 CRC64;

Query Match          51.4%; Score 38; DB 1; Length 256;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YIKANSKEFIGITEL 15
DB 89 YINNSRVVGIGE 102

Search completed: October 10, 2002, 16:04:53
```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 4.83434 Seconds  
(without alignments)  
536.769 Million cell updates/sec

Title: US-09-787-126-34  
Perfect score: 74  
Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

arched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	74	100.0	1310	2 Q93N27	Q93N27 clostridium
2	44.5	60.1	71	7 Q31585	Q31585 salmo salar
3	44.5	60.1	71	7 Q9XRJ9	Q9XRJ9 salvelinus
4	44.5	60.1	85	7 Q95IS2	Q95IS2 salmo salar
5	44.5	60.1	85	7 Q95HY1	Q95HY1 salmo salar
6	44.5	60.1	86	7 Q95HX4	Q95HX4 salmo salar
7	44.5	60.1	244	7 Q31590	Q31590 salmo salar
8	44	59.5	546	10 Q9XG37	Q9XG37 guillardia
9	43.5	58.8	67	7 Q31578	Q31578 salmo salar
10	43	58.1	180	16 Q9CF66	Q9CF66 lactococcus
11	43	58.1	250	9 Q9MCL7	Q9MCL7 streptococ
12	43	58.1	252	9 Q9XJE8	Q9XJE8 lactococcus
13	43	58.1	302	11 Q9CRV4	Q9CRV4 mus musculus
14	43	58.1	309	11 Q9CYD2	Q9CYD2 mus musculus
15	43	58.1	899	12 Q9YTK4	Q9YTK4 ateline her
16	42.5	57.4	1087	5 Q25961	Q25961 plasmodium

17	42.5	57.4	1694	5 Q9NHX1	Q9NHX1 plasmodium
18	42.5	57.4	1694	5 Q9RTZ5	Q9RTZ5 plasmodium
19	42.5	57.4	1704	5 Q9RTZ4	Q9RTZ4 plasmodium
20	42.5	57.4	1720	5 Q25922	Q25922 plasmodium
21	42	56.8	1333	5 Q24262	Q24262 drosophila
22	41.5	56.1	84	13 Q9DEK4	Q9DEK4 coregonus s
23	41.5	56.1	85	7 Q95IS3	Q95IS3 salmo salar
24	41.5	56.1	85	7 Q95IR2	Q95IR2 salmo salar
25	41.5	56.1	149	7 Q31495	Q31495 oncorhynch
26	41.5	56.1	216	7 Q9GJH0	Q9GJH0 salmo trutt
27	41.5	56.1	216	7 Q9GJG9	Q9GJG9 salmo trutt
28	41	55.4	247	11 Q9D3B9	Q9D3B9 mus musculu
29	41	55.4	384	4 Q9HD07	Q9HD07 homo sapien
30	41	55.4	447	16 Q97HK7	Q97HK7 clostridium
31	41	55.4	532	5 Q96671	Q96671 drosophila
32	41	55.4	540	5 Q9VU53	Q9VU53 drosophila
33	40.5	54.7	67	7 Q31577	Q31577 salmo salar
34	40.5	54.7	67	7 Q31581	Q31581 salmo salar
35	40.5	54.7	67	7 Q31582	Q31582 salmo salar
36	40.5	54.7	71	7 Q9XRH1	Q9XRH1 salvelinus
37	40.5	54.7	71	7 Q9XRH6	Q9XRH6 salvelinus
38	40.5	54.7	84	13 Q9DEJ6	Q9DEJ6 coregonus s
39	40.5	54.7	85	7 Q95IS9	Q95IS9 salmo salar
40	40.5	54.7	85	7 Q95IS8	Q95IS8 salmo salar
41	40.5	54.7	85	7 Q95IS6	Q95IS6 salmo salar
42	40.5	54.7	85	7 Q95IS5	Q95IS5 salmo salar
43	40.5	54.7	85	7 Q95HY2	Q95HY2 salmo salar
44	40.5	54.7	85	7 Q95HY0	Q95HY0 salmo salar
45	40.5	54.7	85	7 Q95HX9	Q95HX9 salmo salar

#### ALIGNMENTS

##### RESULT 1

Q93N27 PRELIMINARY; PRT; 1310 AA.  
ID AC Q93N27;  
DT 01-DEC-2001 (TREMREL. 19, Created)  
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE TETANUS TOXIN (FRAGMENT).  
OS Clostridium tetani.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shumin Z., Dianliang L.;  
RT \*Cloning and sequence analysis of tetanus toxin gene.\*;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF389424; AAK72964.2;  
FT NON\_TER 1  
FT NON\_TER 1310 1310  
SQ SEQUENCE 1310 AA; 150316 MW; 9EADDC914418E450 CRC64;

Query Match 100.0%; Score 74; DB 2; Length 1310;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

|||||

DB 831 QYIKANSKFIGITEL 845

##### RESULT 2

Q31585 PRELIMINARY; PRT; 60 AA.

ID Q31585

AC Q31585

DT 01-NOV-1996 (TREMREL. 01, Created)

DT 01-NOV-1996 (TREMREL. 01, Last sequence update)

DT 01-DEC-2001 (TREMREL. 19, Last annotation update)

DE (DB02) MHC CLASS II BETA 1 (FRAGMENT).

```

OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
FT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L24953; AAA49597.1;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6776 MW; 5D4F3449060940E2 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 60;
Best Local Similarity 55.6%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 16 EYIRFNSVGVKFGVGYTEL 33

RESULT 3
Q9XRJ9 PRELIMINARY; PRT; 71 AA.
AC Q9XRJ9;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC CLASS II BETA 1 (FRAGMENT).
GN SANA.
OS Salvelinus namaycush (lake trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8040;
RN [1]
RP SEQUENCE FROM N.A.
RA Dorschner M.O., Duris T., Phillips R.B.;
RT "Diversity of a Lake Trout Mhc class II Gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF130026; AAD20889.1;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 71
SQ SEQUENCE 71 AA; 8002 MW; E3095286582A9F2D CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 71;
Best Local Similarity 55.6%; Pred. No. 1.4;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 14 EYIRFNSVGVKFGVGYTEL 31

RESULT 4
Q95IS2 PRELIMINARY; PRT; 85 AA.
AC Q95IS2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

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DE MHC CLASS II BETA CHAIN (FRAGMENT).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Landry C., Bernatchez L.;
RT "Comparative analysis of population structure across environments and
FT geographic scales at Major Histocompatibility Complex and
RL microsatellite in Atlantic salmon (Salmo salar).";
DR EMBL; AF373699; AAK61882.1;
DR EMBL; AF373699; AAK61882.1;
KW MHC.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9743 MW; 3214E01AD1B66AC5 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 85;
Best Local Similarity 55.6%; Pred. No. 1.7;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 33 EYIRFNSVGVKFGVGYTEL 50

RESULT 5
Q95HY1 PRELIMINARY; PRT; 85 AA.
AC Q95HY1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
GN DBI.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21383619; PubMed-11491536;
RA Langefors A., Lohm J., von Schantz T.;
RT "Allelic polymorphism in MHC class II B in four populations of
FT Atlantic salmon (Salmo salar).";
RL Immunogenetics 53:329-336(2001).
DR EMBL; AF104370; AAL04002.1;
KW MHC.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9723 MW; 27C9F7931F1F01C4 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 85;
Best Local Similarity 55.6%; Pred. No. 1.7;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 33 EYIRFNSVGVKFGVGYTEL 50

RESULT 6
Q95HX4 PRELIMINARY; PRT; 86 AA.
AC Q95HX4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
GN DBI.

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OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383619; PubMed=11491536;
RA Langefors A., Lohm J., von Schantz T.;
RT "Allelic polymorphism in MHC class II B in four populations of
RT Atlantic salmon (Salmo salar).";
RL Immunogenetics 53:329-336(2001).
DR EMBL; AF104377; AAL04009.1; -
KW MHC.
FT NON_TER 1 86
FT NON_TER 86
SQ SEQUENCE 86 AA; 9312 MW; E5097729F681F149 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 86;
Best Local Similarity 55.6%; Pred. No. 1.7;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 33 EYIRFNSTVGKFGVGYTEL 50

RESULT 7
Q31590 PRELIMINARY; PRT; 244 AA.
AC Q31590;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC CLASS II.
GN MHC-SASA CLASS II B.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93170890; PubMed=8436418;
RA Grimholt I., Grimholt U., Fosse V.M., Lie Y., Endresen C.;
RT "Cloning and sequence analysis of cDNAs encoding the MHC class II a-
RT chain in Atlantic salmon, Salmo salar.";
RL Immunogenetics 37:437-441(1993).
DR EMBL; X70166; CAA49725.1; -
DR HSSP; P01888; 1BMG.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; Igcl; 1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 244 AA; 27449 MW; 496CB9EA9D73765C CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 244;
Best Local Similarity 55.6%; Pred. No. 5.1;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 51 EYIRFNSTVGKFGVGYTEL 68

RESULT 8
Q31578 PRELIMINARY; PRT; 67 AA.
AC Q31578;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE (DB03) MHC CLASS II BETA 1 (FRAGMENT).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
RT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L24929; AAA49590.1; -
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 67
FT NON_TER 67
SQ SEQUENCE 67 AA; 7449 MW; 42771AEDBABA6626 CRC64;

Query Match 58.8%; Score 43.5; DB 7; Length 67;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 16 EYIRFNSTVGKFGVGYTEL 33

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AC Q9XG37;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 66.2 KDA PROTEIN.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087226; PubMed=10618395;
RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
RA Cavalier-Smith T., Maier U., Douglas S.;
RT "Chloroplast protein and centrosomal genes, a tRNA intron, and odd
RT telomeres in an unusually compact eukaryotic genome, the cryptomonad
RT nucleomorph.";
RL Nature 410:1091-1096(2001).
DR EMBL; AJ010592; CAB40403.1; -
KW Hypothetical protein.
SQ SEQUENCE 546 AA; 66218 MW; 7303950F632BE6F2 CRC64;

Query Match 59.5%; Score 44; DB 10; Length 546;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 YIKANSKFIGITEL 15
   :||: ||: ||: |||
Db 445 FIKNSRFMLTEI 458

RESULT 9
Q31578 PRELIMINARY; PRT; 67 AA.
AC Q31578;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE (DB03) MHC CLASS II BETA 1 (FRAGMENT).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
RT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L24929; AAA49590.1; -
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 67
FT NON_TER 67
SQ SEQUENCE 67 AA; 7449 MW; 42771AEDBABA6626 CRC64;

Query Match 58.8%; Score 43.5; DB 7; Length 67;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 16 EYIRFNSTVGKFGVGYTEL 33

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## RESULT 10

Q9CF66 PRELIMINARY; PRT; 180 AA.  
 AC Q9CF66; 17, Created  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DE 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE SPERMIDINE ACETYLTRANSFERASE (EC 2.3.1.57).  
 GN YOFF.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Lactococcus.  
 OX NCBI\_TaxID=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IL1403;  
 RX MEDLINE=21235186; PubMed=11337471;  
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
 lactis ssp. lactis IL1403";  
 LA ENBL; AE006391; AAK05713.1;  
 DR InterPro; IPR000182; Acetyltransf\_GCN5.  
 DR Pfam; PF00583; Acetyltransf.1.  
 KW Transferase; Complete proteome.  
 SQ SEQUENCE 180 AA; 21022 MW; 6BBD148524C0DF3C CRC64;

Query Match 58.1%; Score 43; DB 16; Length 180;  
 Best Local Similarity 69.2%; Pred. No. 6.9;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

## Query 3 IKANSKFIGITEL 15

I:|||||  
 65 IEANDTFIGIVEL 77

## RESULT 11

Q9MCL7 PRELIMINARY; PRT; 250 AA.  
 AC Q9MCL7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ORF13.  
 GN ORF13.  
 OS Streptococcus thermophilus bacteriophage 7201.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
 OX NCBI\_TaxID=112023;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20088830; PubMed=10620678;  
 RA Stanley E., Walsh L., van der Zwet A., Fitzgerald G.F.,  
 RA van Sinderen D.;  
 RT "Identification of four loci isolated from two Streptococcus  
 thermophilus phage genomes responsible for mediating bacteriophage  
 resistance";  
 RT FEMS Microbiol. Lett. 182:271-277 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF145054; AAF43506.1;  
 DR InterPro; IPR002295; D21N6\_mtfase.  
 DR InterPro; IPR001091; N4\_Mtase.  
 DR Pfam; PF01555; N6\_N4\_Mtase.1.  
 DR PRINTS; PR00506; D21N6MTFRASE.  
 DR PRINTS; PR00508; S21N4MTFRASE.  
 SQ SEQUENCE 250 AA; 28744 MW; 725EA3B2B56B0D7F CRC64;

Query Match 58.1%; Score 43; DB 9; Length 250;

Best Local Similarity 57.1%; Pred. No. 9.7;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

## Query 1 QYIKANSKFIGITE 14

I:|||||  
 131 QVLKANKMIVGATE 144

## RESULT 12

Q9XJE8 PRELIMINARY; PRT; 252 AA.  
 AC Q9XJE8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PUTATIVE METHYLASE.  
 OS Lactococcus lactis bacteriophage Tuc2009.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
 OX NCBI\_TaxID=35241;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Sinderen D., van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F.;  
 RT "Molecular analysis of the temperate lactococcal phage Tuc2009";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF109874; AAD37103.1;  
 DR InterPro; IPR002295; D21N6\_mtfase.  
 DR InterPro; IPR001091; N4\_Mtase.  
 DR InterPro; IPR002941; N6\_N4\_Mtase.  
 DR Pfam; PF01555; N6\_N4\_Mtase.1.  
 DR PRINTS; PR00506; D21N6MTFRASE.  
 DR PRINTS; PR00508; S21N4MTFRASE.  
 KW Methyltransferase.  
 SQ SEQUENCE 252 AA; 29357 MW; 4D5A59FF47363948 CRC64;

Query Match 58.1%; Score 43; DB 9; Length 252;  
 Best Local Similarity 57.1%; Pred. No. 9.8;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

## Query 1 QYIKANSKFIGITE 14

I:|||||  
 130 QVLKANKMIVGATE 143

## RESULT 13

Q9CRV4 PRELIMINARY; PRT; 302 AA.  
 AC Q9CRV4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 3110030A04RIK PROTEIN (FRAGMENT).  
 GN 3110030A04RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRONIC HEAD;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Barsh G.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK014093; BAB29151.1; -
DR HSP: Q02410; 1AQC
DR MGD: MGI:1920407; j110030A04Rik.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000050; PID_domain.
DR Pfam: PF00640; PID; 1.
DR SMART: SM00462; PTB; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR PROSITE: PS01179; PID; 1.
FT NON_TER 1
FT SEQUENCE 302 AA; 34207 MW; 8CB11440F898C65A CRC64;
Query Match 58.1%; Score 43; DB 11; Length 302;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 YIKANSKFIGITEL 15
DB 22 YIPYNAKFLGSTE 35
II I:II:II:
II I:II:II:
RESULT 14
QYCYD2 PRELIMINARY; PRT; 309 AA.
AC Q9CYD2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 5730529006RIK PROTEIN.
GN 5730529006RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRIO;
RX MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK017798; BAB30939.1; -
DR HSP: Q02410; 1AQC
DR MGD: MGI:1917926; 5730529006RIK.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000050; PID_domain.
DR Pfam: PF00640; PID; 1.
DR SMART: SM00462; PTB; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
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DR PROSITE: PS01179; PID; 1.
SQ SEQUENCE 309 AA; 35272 MW; 535DD8E733C0F406 CRC64;
Query Match 58.1%; Score 43; DB 11; Length 309;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 YIKANSKFIGITEL 15
DB 24 YIPYNAKFLGSTE 37
II I:II:II:
II I:II:II:
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QYCYD4 PRELIMINARY; PRT; 899 AA.
AC Q9YTK4;
AC Q9YTK4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF 63.
OS Ateline herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=85618;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=73;
RX MEDLINE=20091363; PubMed=10623770;
RA Albrecht J.C.;
RT "Primary structure of the Herpesvirus Ateles genome.";
RL J. Virol. 74:1033-1037(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=73;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF083424; AAC95587.1; -
SQ SEQUENCE 899 AA; 103389 MW; 19440A7944DE2531 CRC64;
Query Match 58.1%; Score 43; DB 12; Length 899;
Best Local Similarity 64.3%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 QYIKANSKFIGITE 14
DB 124 QYITNSTFTGQPE 137
II I:II:II:II:II:II:
II I:II:II:II:II:II:
Search completed: October 10, 2002, 16:03:02
Job time : 6.83434 secs
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 1.80723 Seconds  
(without alignments)  
202.732 Million cell updates/sec

Title: US-09-787-126-34  
Perfect score: 74  
Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	2	US-08-319-704-10
2	74	100.0	15	2	US-08-661-052-6
3	74	100.0	15	2	US-08-460-502-7
4	74	100.0	15	4	US-09-046-373-2
5	74	100.0	15	4	US-09-188-082-6
6	74	100.0	15	5	PCT-US93-11703-69
7	74	100.0	16	4	US-09-248-588-55
8	74	100.0	17	1	US-08-446-692-4
9	74	100.0	17	2	US-08-488-351A-4
10	74	100.0	17	3	US-09-100-409A-40
11	74	100.0	17	5	PCT-US95-08596-23
12	74	100.0	17	5	PCT-US95-13841-7
13	74	100.0	27	1	US-08-446-692-13
14	74	100.0	27	2	US-08-488-351A-13
15	74	100.0	31	5	PCT-US93-11703-63
16	74	100.0	37	1	US-08-446-692-57
17	74	100.0	37	1	US-08-446-692-63
18	74	100.0	37	2	US-08-488-351A-57
19	74	100.0	37	2	US-08-488-351A-63
20	74	100.0	47	1	US-08-446-692-35
21	74	100.0	47	2	US-08-488-351A-35
22	70	94.6	14	1	US-08-186-266-5
23	70	94.6	14	1	US-08-305-871A-5
24	70	94.6	14	1	US-08-465-167A-18
25	70	94.6	14	2	US-08-817-933A-9
26	70	94.6	14	5	PCT-US92-07218-15
27	70	94.6	14	5	PCT-US92-07218-30

Sequence 95, Appl  
Sequence 25, Appl  
Sequence 31, Appl  
Sequence 110, Appl  
Sequence 26, Appl  
Sequence 27, Appl  
Sequence 28, Appl  
Sequence 32, Appl  
Sequence 111, Appl  
Sequence 112, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 29, Appl  
Sequence 9, Appl  
Sequence 7, Appl  
Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-08-319-704-10  
; Sequence 10, Application US/08319704  
; Patent No. 5814617  
; GENERAL INFORMATION:  
; APPLICANT: Hoffman, Stephen L.  
; APPLICANT: Charoenvit, Yupin  
; APPLICANT: Hedstrom, Richard C.  
; APPLICANT: Doolan, Denise L.  
; TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and  
; TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene  
; NUMBER OF SEQUENCE ADDRESSES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Naval Medical R & D Command  
; STREET: Bldg 1, T-12, 8901 Wisconsin Avenue  
; CITY: Bethesda  
; STATE: Maryland  
; COUNTRY: U.S.A  
; ZIP: 20889-5606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/319,704  
; FILING DATE: 07-OCT-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. David Spevack  
; REGISTRATION NUMBER: 24,743  
; REFERENCE/DOCKET NUMBER: 75,206  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 295-6759  
; TELEFAX: (301) 295-1022  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-319-704-10

Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15

RESULT 2  
US-08-661-052-6  
; Sequence 6, Application US/08661052  
; Patent No. 5837243  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano  
; APPLICANT: Chezhian Somasundaram  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD  
; TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,052  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,172  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MX1-043CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal  
; US-08-661-052-6  
Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 3  
US-08-460-502-7  
; Sequence 7, Application US/08460502  
; Patent No. 5843464  
; GENERAL INFORMATION:  
; APPLICANT: Bakaletz, Lauren O.  
; APPLICANT: Kawaya, Parvin T.  
; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides  
; NUMBER OF SEQUENCES: 11.  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calfee, Halter and Griswold  
; STREET: 800 Superior Avenue  
; CITY: Cleveland  
; STATE: Ohio  
; COUNTRY: U.S.A.  
; ZIP: 44114-2688  
Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 4  
US-09-046-373-2  
; Sequence 2, Application US/09046373  
; Patent No. 6235714  
; GENERAL INFORMATION:  
; APPLICANT: Sudhir Paul  
; APPLICANT: Larry J. Smith  
; APPLICANT: Gennady Gololobov  
; TITLE OF INVENTION: Methods for Identifying Inducers and  
; TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: UNMC 63123  
; CURRENT APPLICATION NUMBER: US/09/046,373  
; CURRENT FILING DATE: 1998-03-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Clostridium tetani  
; US-09-046-373-2  
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Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 5  
US-09-188-082-6  
; Sequence 6, Application US/09188082  
; Patent No. 6270765  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,502  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Golrick, Mary E.  
; REGISTRATION NUMBER: 34,829  
; REFERENCE/DOCKET NUMBER: 22727/00120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216) 622-8458  
; TELEFAX: (216) 241-0816  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-460-502-7  
Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 4  
US-09-046-373-2  
; Sequence 2, Application US/09046373  
; Patent No. 6235714  
; GENERAL INFORMATION:  
; APPLICANT: Sudhir Paul  
; APPLICANT: Larry J. Smith  
; APPLICANT: Gennady Gololobov  
; TITLE OF INVENTION: Methods for Identifying Inducers and  
; TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: UNMC 63123  
; CURRENT APPLICATION NUMBER: US/09/046,373  
; CURRENT FILING DATE: 1998-03-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Clostridium tetani  
; US-09-046-373-2  
Query Match 100.0%; Score 74; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 5  
US-09-188-082-6  
; Sequence 6, Application US/09188082  
; Patent No. 6270765  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano



APPLICANT: Chezian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-PC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-09-188-082-6  
Query Match 100.0%; Score 74; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 6  
PCT-US93-11703-69  
US-09-188-082-6  
GENERAL INFORMATION:  
APPLICANT: Chiron Mimotopes Pty. Ltd.  
TITLE OF INVENTION: T-Cell Epitopes  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grant D. Green  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11703  
FILING DATE: 28-DEC-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/984,852  
FILING DATE: 02-DEC-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D.  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0222.101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2706  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-11703-69  
Query Match 100.0%; Score 74; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 7  
US-09-248-588-55  
US-09-248-588-55  
GENERAL INFORMATION:  
APPLICANT: Birkett, Ashley J.  
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and  
their Derivatives  
FILE REFERENCE: SYN-101 4564/69529  
CURRENT APPLICATION NUMBER: US/09/248,588  
CURRENT FILING DATE: 1999-02-11  
EARLIER FILING DATE: 1998-02-12  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 55  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Clostridium tetani  
PUBLICATION INFORMATION:  
JOURNAL: Vaccine  
VOLUME: 15  
ISSUE: 4  
PAGES: 377-  
DATE: 1997  
US-09-248-588-55  
Query Match 100.0%; Score 74; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 8  
US-08-446-692-4  
US-08-446-692-4  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
and synthetic universal immune stimulators for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-692-4

Query Match 100.0%; Score 74; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIGITEL 15  
| | | | | | | | | | | | | | | | |  
Db 3 QYKANSKFIGITEL 17

RESULT 9  
US-08-488-351A-4  
Sequence 4, Application US/08488351A  
Patent No. 5843446  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,351A  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-4

Query Match 100.0%; Score 74; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIGITEL 15  
| | | | | | | | | | | | | | | | |  
Db 3 QYKANSKFIGITEL 17

RESULT 10  
US-09-100-409A-40  
Sequence 40, Application US/09100409A  
Patent No. 6090388  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Yi  
TITLE OF INVENTION: PEPTIDE COMPOSITION FOR  
TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND  
TITLE OF INVENTION: IMMUNE DISORDERS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,409A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 1151-4154  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-100-409A-40

Query Match 100.0%; Score 74; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYIRANSKFIGITEL 15  
Db 3 QYIRANSKFIGITEL 17

## RESULT 11

PCT-US95-08596-23  
; Sequence 23, Application PC/TUS9508596

## GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Proinsulin Peptide Compounds for Detecting

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08596

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,220

FILING DATE: 08-JULY-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A., Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: DCI-092PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

PCT-US95-08596-23

Query Match 100.0%; Score 74; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYIRANSKFIGITEL 15  
Db 3 QYIRANSKFIGITEL 17

## RESULT 12

PCT-US95-13841-7

; Sequence 7, Application PC/TUS9513841

## GENERAL INFORMATION:

APPLICANT: United Biomedical Inc; Walfield, Alan M.;

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Synthetic Ige Membrane Anchor

TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13841

FILING DATE: 25-OCT-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/328,519

FILING DATE: 25-OCT-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lin, Maria C.H.

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4117

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-13841-7

Query Match 100.0%; Score 74; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYIRANSKFIGITEL 15  
Db 3 QYIRANSKFIGITEL 17

## RESULT 13

US-08-446-692-13

; Sequence 13, Application US/08446692

Patent No. 5759551

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

APPLICANT: Zamb, Timothy

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-692-13

Query Match 100.0%; Score 74; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYIKANSKFIGITEL 15  
DB 3 QYIKANSKFIGITEL 17

RESULT 14  
US-08-488-351A-13  
Sequence 13, Application US/08488351A  
Patent No. 5843446  
GENERAL INFORMATION:

APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulants for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US

ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-13

Query Match 100.0%; Score 74; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYIKANSKFIGITEL 15  
DB 3 QYIKANSKFIGITEL 17

RESULT 15  
PCT-US93-11703-63  
Sequence 63, Application PC/TUS9311703  
GENERAL INFORMATION:

APPLICANT: Chiron Mimotopes Pty. Ltd.  
TITLE OF INVENTION: T-Cell Epitopes  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grant D. Green  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.308  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11703  
FILING DATE: 28-DEC-1993  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/984,852  
FILING DATE: 02-DEC-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D.

REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0222.101

TELEPHONE: 510-601-2706  
TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-11703-63

Query Match 100.0%; Score 74; DB 5; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYIKANSKFIGITEL 15  
DB 10 QYIKANSKFIGITEL 24

Search completed: October 10, 2002, 16:03:56  
Job time: 2.80723 secs